



#14

SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA
Akio MATSUDA
Goichi HONDA
Shuji MURAMATSU
Yukiko NAGANO

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Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
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Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
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Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
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Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
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 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
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 Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
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 Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
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 Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
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 Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
 85 90 95
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Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
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Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
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aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
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Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
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Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
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115 120 125
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Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
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Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
165 170 175
Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly
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Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser
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Met Ala Gly Ala
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Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
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Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
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Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
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Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
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Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85 90 95 100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572
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120 125 130

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 Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His
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 Val Phe His Arg Val
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 Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
 50 55 60
 Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
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 Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
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 Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
 115 120 125
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 130 135 140
 Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
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 Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
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Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
 170 175 180 185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689
 Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
 190 195

ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749
 gctgggttttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact 809
 ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acatttttaa 869
 aagcacacag ctcaaagtca gccataaagt cttttcctat ttgtgacttt tactaataaa 929
 aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc 989
 accacatagt tttaacttga ctttcaagat aattttcagg gtttttggtg ttgttggttt 1049
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 atgcctgggtg gcttttcaca aaaagcagat tttcttcatg tactgtgatg tctgatgcaa 1349
 tgcatectag aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg 1409
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 ttgcaataaa gaaattttat tttaaacc 1498

<210> 11
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Ala Leu Ala Leu Ala Ala Leu Ala Val Glu Pro Ala Cys Gly
 1 5 10 15
 Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu
 20 25 30
 Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu
 35 40 45
 Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
 50 55 60
 Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
 65 70 75 80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu 95
 85
 Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile 110
 100 105
 Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe 125
 115 120
 Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala 140
 130 135
 Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp 160
 145 150 155
 Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly 175
 165 170
 Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe 190
 180 185
 Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr 205
 195 200
 Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr 220
 210 215

<210> 12
 <211> 1864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (153)..(815)

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 cccctcggcc tcccagcgct cccaagccgc agcggccgcg ccccttcagc tagctcgctc 120
 gctcgctctg cttccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173
 Met Ala Leu Ala Leu Ala Ala 5
 1
 ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221
 Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln 20
 10 15
 aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269
 Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro 35
 25 30
 cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317
 Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr 55
 40 45 50

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365
Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr 70
60

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413
Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr 85
75

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp 100
90

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509
Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met 115
105

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557
Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu 135
120

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605
Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser 150
140

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653
Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser 165
155

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701
Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val 180
170

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749
Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr 195
185

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797
Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr 215
200

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg 845
Arg Val Leu Phe Ile Tyr 220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca 905
gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc 965
tctctatttg ttcttaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025
atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085
gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145
ggggcagtct tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

gatatgtata atgctggcca ttttaaaggg gttttctcaa aagttaaact ttgctatga 1265
 ctgtgttttt gcacataatc catatttgct gttcaagtta atctagaaat ttattcaatt 1325
 ctgtatgaac acctggaagc aaaatcatag tgcaaaaata catttaaggt gtgggtcaaaa 1385
 ataagtcttt aattggtaaa taataagcat taatttttta tagcctgtat tcacaattct 1445
 gcggtacctt attgtaccta agggattcta aagggtgtgt cactgtataa aacagaaagc 1505
 actaggatac aaatgaagct taattactaa aatgtaattc ttgacactct ttctataatt 1565
 agcgttcttc acccccaccc ccacccccac ccccttatt ttcttttgt ctctggtga 1625
 ttaggcaaaa gtctgggagt aaggagagga ttaggtactt aggagcaaag aaagaagtag 1685
 cttggaactt ttgagatgat ccctaacata ctgtactact tgcttttaca atgtgttagc 1745
 agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtggg aattcatctt 1805
 ggtttgctat gttaaaactg taaatacaac agaacattaa taaatatctc ttgtgtagc 1864

<210> 13
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 13
 Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
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 Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
 20 25 30
 Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu
 35 40 45
 Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
 50 55 60
 Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
 65 70 75 80
 Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
 85 90 95
 Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln
 100 105 110
 Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
 115 120 125
 Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
 130 135 140
 Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile

145 150 160
 Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
 165 170 175
 Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
 180 185 190
 Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
 195 200 205
 Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
 210 215 220
 Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
 225 230 235 240
 Leu Leu

<210> 14
 <211> 2324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(738)

<400> 14
 gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51
 Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
 1 5 10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99
 Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
 15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147
 Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala
 30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
 Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
 50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
 Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
 65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291
 Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
 80 85 90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339
 Glu Ala Glu Lys Ala Lys Ala Ala Met Ala Ala Ala Ala Ala Glu

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
 Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe 125
 110 115 120

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
 Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu 140
 130 135

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
 Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser 155
 145 150

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
 Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly 170
 160 165

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp 185
 175 180

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
 Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe 205
 190 195 200

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675
 Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu 220
 210 215

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
 Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg 235
 225 230

tat ttc ttc tta ttg tagagactgc atcaaccgga cattcctttc ttataccaat 778
 Tyr Phe Phe Leu Leu 240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838
 gacaaattag tgaagaaaag acggagtttc gaaattgaat ggaggggtgg tttttgctta 898
 caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata 958
 tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018
 tccagtcaca tttgggtaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078
 tcttccagct tgtaaagcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138
 ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198
 atgaaacatc ttttggtata taggggtgat tgaaacctgc agtgctgatt attagaaagg 1258
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actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatatata 1438
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 aagagatctt gcaggaagag attgtattag atattatatt ttttcattt aagataattt 1678
 tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738
 aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798
 ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858
 acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918
 gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978
 aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038
 tctgtttttc ctttcgggta tatctttgggt tttgaatacc aacatttaaa atgatggat 2098
 tttatctttt aaacttaaaa attatttaat acagctatat ggacctata aaattgattt 2158
 cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218
 catttccaaa aaataaaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278
 cattgtcttt gataaataaa acagttttgt tttgctaata tagcct 2324

<210> 15
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
 1 5 10 15
 Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
 20 25 30
 Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu
 35 40 45
 Glu Thr Asp Ser Ser Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
 50 55 60
 Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
 65 70 75 80
 Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
 85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln
 100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
 115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
 130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
 145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
 165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
 180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
 195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
 210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
 225 230 235 240

Leu Leu

<210> 16
 <211> 2324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(738)

<400> 16
 gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51
 Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
 1 5 10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99
 Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
 15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147
 Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala
 30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
 Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
 50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
 Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
 65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291
 Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
 80 85 90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339
 Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu
 95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
 Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
 110 115 120 125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
 Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
 130 135 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
 Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
 145 150 155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
 Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
 160 165 170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
 175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
 Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
 190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675
 Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
 210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
 Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
 225 230 235

tat ttc ttc tta ttg tagagactgc atcaaccgga cattcctttc ttataccaat 778
 Tyr Phe Phe Leu Leu
 240

gtgaaatttc cagatcatct gtaaaccctac aactttaata gaagactact aataacagaa 838

gacaaatttag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc ttttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078
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 ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198
 atgaaacatc ttttgttata taggggtgtat tgaaacctgc agtgctgatt attagaaagg 1258
 atttgtcaga tttttgaaca tgatatTTac attattattt aggaaaactc ttcttgtaaa 1318
 taaccatgca taacttactt tctgcaatgt tttcttagaa atttgttcca gatagctttc 1378
 actaatTTta aattaagtga actaaatata tatgtgtata tgtatacaca tatatatata 1438
 cacacacata tatatatTTa gaaacgtgag tgtaaagat agaatttgtt ttaggacaaa 1498
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 aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678
 tcaaagttaa ttttctaaat aagataattc tcatttTgtt ttgtctTTta aaaggccaat 1738
 aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttTtaa agcttagcaa 1798
 ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858
 acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttTgtg 1918
 gcatatagga ctgtggggTc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978
 aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038
 tctgtttttc ctttcggTta tatctttTgt tttgaatacc aacattTtaa atgatggTat 2098
 tttatctttt aaactTaaaa attattTaat acagctatat ggaccttata aaattgattt 2158
 cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218
 catttccaaa aaataaaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278
 cattgtcttt gataaataaa acagtTTTgt tttgctaata tagcct 2324

<210> 17
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
 1 5 10 15
 Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
 20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
 35 40 45
 Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
 50 55 60
 Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
 65 70 75 80
 Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
 85 90 95
 His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
 100 105 110
 Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
 115 120 125
 Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr
 130 135 140
 Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
 145 150 155 160
 Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
 165 170 175
 Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
 180 185 190
 Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
 195 200 205
 Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
 210 215 220
 Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
 225 230 235 240
 Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
 245 250 255
 Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
 260 265 270
 Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
 275 280 285
 Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
 290 295 300
 Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
 305 310 315 320
 Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
 325 330 335

<210> 18
 <211> 2636
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(1060)

<400> 18
 cttacttttc catctcctcc caccagcta taccctccca ctggcggcgc gg atg gca 58
 Met Ala
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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106
 Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
 5 10 15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
 Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
 20 25 30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202
 Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35 40 45 50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
 Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Arg Gly Pro Ala Ala
 55 60 65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser

165 170 175
 gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
 Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
 180 185 190
 gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
 Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
 195 200 205
 gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
 Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
 215 220 225
 gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778
 Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
 230 235 240
 ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826
 Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
 245 250 255
 gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
 Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
 260 265 270
 tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
 Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
 275 280 285 290
 gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970
 Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
 295 300 305
 ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
 Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
 310 315 320
 agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
 Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
 325 330 335
 tagagactgc atcaaccgga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120
 gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180
 acggagtttc gaaattgaat ggcaggggtgg tttttgctta caagccattt ctgttcattc 1240
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 gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360
 cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaatgcc 1420
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taagggtgat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca 1600
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 accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900
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 attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500
 actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaaatt 2560
 tattatgctt tataacctct tctgtatttt ctaatttttt cattgtcttt gataaataaa 2620
 acagttttgt tttgct 2636

<210> 19
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 19
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 1 5 10 15
 Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
 20 25 30
 Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
 35 40 45
 Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
 50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
 65 70 75 80
 Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
 85 90 95
 His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
 100 105 110
 Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
 115 120 125
 Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
 130 135 140
 Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
 145 150 155 160
 Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
 165 170 175
 Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
 180 185 190
 Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
 195 200 205
 Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
 210 215 220
 Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
 225 230 235 240
 Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
 245 250 255
 Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
 260 265 270
 Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
 275 280 285
 Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
 290 295 300
 Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
 305 310 315 320
 Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
 325 330 335

<210> 20
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (53)..(1060)

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 Met Ala

1

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 Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
 5 10 15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
 Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
 20 25 30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202
 Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35 40 45 50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
 Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
 55 60 65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Tyr Ser
 165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
 Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
 180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
 Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu 210
 195 200 205

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
 Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg 225
 215 220

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778
 Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile 240
 230 235

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826
 Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile 255
 245 250

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
 Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys 270
 260 265

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
 Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn 290
 275 280 285

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970
 Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu 305
 295 300

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
 Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu 320
 310 315

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
 Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu 335
 325 330

tagagactgc atcaaccgga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120
 gtaaaccctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180
 acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240
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tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaatTTta aattaagtga 1720
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 gaaacgtgag tgTTaaagat agaatttgTT ttaggacaaa tTTtaagaaa atgtgggaat 1840
 accaaatgtc cTTtataaga aaaataaatt ttgtTTtaag ggacatacca gTTtttaggga 1900
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 attgtattag atattatatt tatttcattt aagataattt tcaaagttaa tTTtctaaat 2020
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 tgcaaaatac tcattttcaa gTTatggaaa tgtgtttgtg gcatatagga ctgtggggTc 2260
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 attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500
 actactaaaa ggtacatcta actattcagg gacattTTTc catttccaaa aaataaaatt 2560
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 acagttttgt tttgct 2636

<210> 21
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 21
 Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr
 1 5 10 15
 Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val
 20 25 30
 Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn
 35 40 45
 Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr
 50 55 60
 Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
 65 70 75

<220>
<221> CDS
<222> (176)..(403)

32

tataaaattt taatccttac tgcatttctt ctgttcctac aaatgtatta aacatttcagt 1083
1085

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<210> 23
<211> 84
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
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Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
20 25 30
Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45
Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
50 55 60
Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
65 70 75 80
Leu Ser Gly Leu

<210> 24
<211> 1593
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (65)..(316)

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cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109
Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile 15
1 5 10
ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157
Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys 30
20 25 30
gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205
Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln 45
35
att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253
Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301
 Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His
 65 70 75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356
 Ser Leu Ser Gly Leu
 80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggctttagac 416
 attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt 476
 gcgtgcagcc tgctggggag accccactct gtgcacctat tggctcttct agctgactct 536
 tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca 596
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 aaggcaccag gcctcaggag gagccccata gtcccgctg cagcctgtaa ccacggctg 1436
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 tgaataagtg acaaataaag ccagtttttt acaaggt 1593

<210> 25

<211> 179

<212> PRT

<213> Homo sapiens

<400> 25
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 1 5 10 15
 Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
 20 25 30
 Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
 35 40 45
 Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
 50 55 60
 Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
 65 70 75 80
 Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
 85 90 95
 Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
 100 105 110
 Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
 115 120 125
 Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
 130 135 140
 Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr
 145 150 155 160
 Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala
 165 170 175
 Leu Leu Phe

<210> 26
 <211> 1820
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (114)..(650)

<400> 26
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 acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116
 Met
 1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164
 Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212
 Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu
 20 25 30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260
 Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro
 35 40 45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308
 Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val
 50 55 60 65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356
 Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr
 70 75 80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404
 Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu
 85 90 95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452
 Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val
 100 105 110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500
 His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Phe Gly Gly Leu
 115 120 125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548
 Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
 130 135 140 145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596
 Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
 150 155 160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644
 Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
 165 170 175

ctc ttc tgagcccgctc tcccggacag gttgaggaag ctgctccaga agcgccctcgg 700
 Leu Phe

aaggggagct ctcatcatgg cgcgtgctgc tgcggcatat ggacttttaa taatgttttt 760

gaatttcgta ttcttttcatt ccactgtgta aagtgtctaga cattttccaa tttaaaattt 820

tgcttttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

tttgcacctt ctcaagtgtg tatgcggtg cagccgtctc acctgtttcc ccacaaaggg 1000

aattttctcac tctggttgga agcacaacaa ctgaaatgtc tacgtttcat tttggcagta 1060

ggggtgtgaag ctgggagcag atcatgtatt tcccggagac atgggacctt gctggcatgt 1120
 ctcccttcaca atcaggcgtg ggaatatctg gcttaggact gtttctctct aagacaccat 1180
 tgttttccct tatttttaaaa gtgatttttt taaggacaga actttttcca aaagagaggg 1240
 atggcctttcc cagaagacac tctggagacc ttgctggcag tgctagccag gaaacagagt 1300
 gaccaaggga caagaaggga cttgcctaaa gccaccagc aactcagcag cagaaccaag 1360
 atggggcccca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggccttgt 1420
 ctagaccag tctgagcag gggagaggct cttgagacct gatgccctcc taccacatg 1480
 gttctccac tgccctgtct gctctgctgc tacaragggg cagggcctcc ccagccccc 1540
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 ctggaaggca ccaggcctca ggaggagccc catagtcccg cctgcagcct gtaaccatcg 1660
 gctggggcct gcaaggccca cactcacgcc ctgtgggtga tggtcacggt ggggtgggtg 1720
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 aaggtgaata agtgacaaat aaagccagtt ttttacaagg 1820

<210> 27
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 27
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 20 25 30
 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60
 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110
 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
 115 120 125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
130 135 140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145 150 155 160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
165 170 175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
180 185 190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
195 200 205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
210 215 220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225 230 235 240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
245 250 255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
260 265 270

Ile Ala Lys Val Lys Ala Asn
275

<210> 28
<211> 1472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119)..(955)

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tgctccctcc gagcgctccg ccgttgcccg cctggcccct acggagtcct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
1 5 10 15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214
Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
20 25 30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262
Ser Ile Leu Leu Thr Tyr Val Phe Val Leu Ser Leu Gly Pro Arg
35 40 45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc	310
Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val	
50 55 60	
tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc	358
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe	
65 70 75 80	
ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg	406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val	
85 90 95	
gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg	454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp	
100 105 110	
ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt	502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe	
115 120 125	
att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat	550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His	
130 135 140	
cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg	598
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro	
145 150 155 160	
gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc	646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val	
165 170 175	
ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa	694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln	
180 185 190	
ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag	742
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln	
195 200 205	
ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc	790
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser	
210 215 220	
tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc	838
Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly	
225 230 235 240	
acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc	886
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr	
245 250 255	
aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt	934
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly	
260 265 270	
att gcc aag gtc aag gcc aac tgagaagcat ggccagata ggcccccacc	985

Ile Ala Lys Val Lys Ala Asn
275

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045
gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct cccacagct 1105
gctctacagg gaccacggct ttggttcctc acccacttcc cccgggcagc tccagggatg 1165
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tcctccaccc cacacactga agcagtagct tctgggccaa aggtcagggt gggcgggggc 1405
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ggaaacc 1472

<210> 29
<211> 137
<212> PRT
<213> Homo sapiens

<400> 29
Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
1 5 10 15
Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
20 25 30
Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
35 40 45
Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
50 55 60
Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
65 70 75 80
Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
85 90 95
Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
100 105 110
Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
115 120 125
Tyr Met Asp Ala Pro Lys Ala Ala Leu
130 135

<210> 30

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<220>
<221> CDS
<222> (145)..(555)
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41

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 accctagggg gaccaagtag ggcctgtcac accaggggtg cgcagctttc tgtgtgatgc 975
 agatgtgtcc tggtttcggc agcgtagcca gctgctgctt gaggccatgg ctctgccccg 1035
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<210> 31
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
 1 5 10 15
 Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
 20 25 30
 Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
 35 40 45
 Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
 50 55 60
 Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 65 70 75 80
 Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Tyr

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
 100 105 110

Glu Cys Pro Cys Gln Leu
 115

<210> 32
 <211> 1908
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(444)

<400> 32
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ggaggcctct ggggtgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114
 Met Gly Phe Gly Ala Thr Leu Ala
 1 5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162
 Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys
 10 15 20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210
 Phe Thr Cys Ser Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg
 25 30 35 40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258
 Pro Val Val Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr
 45 50 55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306
 Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
 60 65 70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354
 Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
 75 80 85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402
 Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
 90 95 100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444
 Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
 105 110 115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcaccat cccaaactac 504

atcactcaac aggcctctgc ccctttctgc ttgcctgcc ctcacacggc agcccacat 564

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 tttataataa atgcaatcgt ttgg 1908

<210> 33
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
 1 5 10 15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro
35 40 45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
50 55 60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
65 70 75 80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
130 135 140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
145 150 155 160

Ser Asp Gly Gly Tyr Thr Ile Trp
165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(573)

<400> 34

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gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111
Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

1

5

10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159
Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro
15 20 25 30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207
Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
35 40 45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
50 55 60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303
 Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
 65 70 75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351
 Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
 80 85 90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399
 Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
 95 100 105 110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
 Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
 115 120 125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
 Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
 130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543
 Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
 145 150 155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593
 Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp
 160 165

tgtgccggga aagacatcac ataccttcag cactttctcac aatgtaactg ctttagtcat 653
 attaacctga agttgcagtt tagacacatg ttgttggggt gtctttctgg tgcccaaact 713
 ttcaggcact tttcaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc 773
 attttgaggt aggggaggta tccattcata aaatgaatgt ggggtgaagcc gccctaagga 833
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 aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta 953
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ggaggatgca tttcaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493
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 ccagaattcc tagactgggt taataggggc atattgtgaa tgtctcacta caaaatgact 1613
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 tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcggt 1793
 gtatgtctct ctctacactg tgggtgcactt aacttgtgga atttttatac taaaaatgta 1853
 gaataaagac tattttgaag atttgaataa agtgatgaag ttgc 1897

<210> 35
 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 35
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 1 5 10 15
 Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
 20 25 30
 Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
 35 40 45
 Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
 50 55 60
 Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
 65 70 75 80
 Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
 85 90 95
 Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
 100 105 110
 Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
 115 120 125
 Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
 130 135 140
 Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
 145 150 155 160
 Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
 165 170 175
 Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg

180

185

190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
195 200 205

Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
210 215 220

Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225 230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
245 250 255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
260 265 270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
275 280 285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
290 295 300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305 310 315 320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
325 330 335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
340 345 350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
355 360 365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
370 375 380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
385 390 395 400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
405 410 415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
420 425 430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
435 440 445

Pro Glu Lys Gln Met Ala Pro
450 455

<210> 36
<211> 1903
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

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tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118
Met
1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166
Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe
5 10 15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214
Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr
20 25 30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262
Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala
35 40 45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310
Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
50 55 60 65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
70 75 80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
85 90 95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser
100 105 110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
115 120 125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe
165 170 175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg 694
 Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu
 180 185 190

ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg 742
 Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met
 195 200 205

gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca 790
 Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser
 210 215 220 225

ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt 838
 Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser
 230 235 240

gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta 886
 Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu
 245 250 255

agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag 934
 Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu
 260 265 270

aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt 982
 Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu
 275 280 285

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc 1030
 Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
 290 295 300 305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga 1078
 Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
 310 315 320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag 1126
 Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
 325 330 335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc 1174
 Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
 340 345 350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc 1222
 Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala
 355 360 365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag 1270
 Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln
 370 375 380 385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt 1318
 Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
 390 395 400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366

Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu
 405 410 415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414
 Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser
 420 425 430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462
 Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro
 435 440 445

gag aag caa atg gca cct tgaacttaag cctactacag actgtagag 1510
 Glu Lys Gln Met Ala Pro
 450 455

gccagtggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570
 ttataaacia acaaaatgct atggtagcat tttcacctt catagcatac tccttccccg 1630
 tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690
 agacaatact cagcagagag catcccggtgt ggatatgagg ctggtgtaga ggcgagagag 1750
 agccaagaaa ctaaagggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810
 gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaaaagggt tatagctttg 1870
 ccttgagatt gactcattaa aatcagagac tgt 1903

<210> 37
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 37
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 1 5 10 15
 Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
 20 25 30
 Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser
 35 40 45
 Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile
 50 55 60
 Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
 65 70 75 80
 His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met
 85 90 95
 Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala
 100 105 110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
 115 120 125
 Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
 130 135 140
 Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu
 145 150 155 160
 Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
 165 170 175
 Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
 180 185 190
 Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe
 195 200 205
 Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
 210 215 220
 Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
 225 230 235 240
 Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
 245 250 255
 Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
 260 265 270
 Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
 275 280 285
 Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
 290 295 300
 Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
 305 310 315 320
 Phe Gln

<210> 38
 <211> 1448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (292)..(1257)

<400> 38
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 ccctgccccg cccctcccc tccgcctcgc ggcgacggcg gcggtggcgg cttggacgac 120

tcggagagacc	gagtgaagac	atttccacct	ggacacctga	ccatgtgcct	gccctgagca	180
gcgaggccca	ccaggcatct	ctgttggtggg	cagcagggcc	aggctctggt	ctgtggaccc	240
tcggcagttg	gcaggctccc	tctgcagtgg	ggtctggggcc	tcggccccac	c atg tcg	297
					Met Ser	
					1	
agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc	345					
Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser						
5 10 15						
acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca	393					
Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala						
20 25 30						
gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca	441					
Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala						
35 40 45 50						
gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt	489					
Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser						
55 60 65						
gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac	537					
Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr						
70 75 80						
tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc	585					
Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly						
85 90 95						
gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg	633					
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu						
100 105 110						
ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc	681					
Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser						
115 120 125 130						
aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc	729					
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser						
135 140 145						
aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg	777					
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu						
150 155 160						
cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag	825					
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu						
165 170 175						
cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag	873					
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu						
180 185 190						
gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac	921					

Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
 195 200 205 210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969
 Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
 215 220 225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017
 Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
 230 235 240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065
 Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
 245 250 255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113
 Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
 260 265 270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161
 Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
 275 280 285 290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209
 Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
 295 300 305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257
 Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
 310 315 320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcaccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctgtt tttatatata tattttttgt tgtcgtttta acatctccac 1437

gtccctagca t 1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn
 1 5 10 15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His
 20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu
 35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys
 50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu
65 70 75 80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
85 90 95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
100 105 110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
115 120 125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
130 135 140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
145 150 155 160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
165 170 175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
180 185 190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
195 200 205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
210 215 220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
290 295 300

Gln Met His Ile Trp Met Ser Ser Thr
305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(1091)

<400> 40

ggcgggaaccg agctgacggg cgtgcgggccg ctgcgccgca aactcgtgtg ggacgcaccg 60

ctccagccgc ccgcgggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173
Met Ala Gly Gln Pro Gly His
1 5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221
Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro
10 15 20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269
Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg
25 30 35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317
Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln
40 45 50 55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val
60 65 70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg
75 80 85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro
90 95 100

aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac 509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn
105 110 115

att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag 557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys
120 125 130 135

tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag 605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys
140 145 150

tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg 653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg
155 160 165

gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg 701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
170 175 180

ggc gtc gtg aag ctc ggt gac ctt ggt ctg gcc cgc ttc ttc agc tct 749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser

185

190

195

gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca 797
 Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser
 200 205 210 215

 ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845
 Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp
 220 225 230

 tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893
 Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe
 235 240 245

 tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941
 Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln
 250 255 260

 tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989
 Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg
 265 270 275

 gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037
 Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
 280 285 290 295

 atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085
 Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
 300 305 310

 agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgcottac 1141
 Ser Thr

 ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggg 1201

 tcagcaggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261

 agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

 gttgtggaca atctcagctg ggtcaataag ggcaggtggg tcagcgagcc acggcagccc 1381

 cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441

 tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501

 ttagtaccgg gttcagttta gttcttggtg tcttttcaat caagctgtgt gcttaattta 1561

 ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro

1 5 10 15
 Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr
 20 25 30
 Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
 35 40 45
 Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
 50 55 60
 Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
 65 70 75 80
 Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
 85 90 95
 Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
 100 105 110
 Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
 115 120 125
 Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
 130 135 140
 Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
 145 150 155 160
 Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
 165 170 175
 Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
 180 185 190
 Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
 195 200 205
 Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
 210 215 220
 Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
 225 230 235 240
 Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
 245 250 255
 Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
 260 265 270
 Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
 275 280 285
 Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
 290 295 300
 Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe

305

310

315

320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
 325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
 340 345 350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
 355 360 365

Ala Lys Glu
 370

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

attggccatc accgcgcggc cgcgccagcgg acaccgtgcg taccggcctg cggcgcccgg 60

ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114
 Met Ser His Glu Lys Ser Phe Leu
 1 5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162
 Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly
 10 15 20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210
 Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
 25 30 35 40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258
 Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
 45 50 55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306
 Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
 60 65 70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354
 Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
 75 80 85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402
 Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
 90 95 100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450
 Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe

105

110

115

120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498
 Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
 125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546
 Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
 140 145 150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg 594
 Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val
 155 160 165

ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act 642
 Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr
 170 175 180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac 690
 Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr
 185 190 195 200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt 738
 Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys
 205 210 215

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg 786
 Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser
 220 225 230

gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc 834
 Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe
 235 240 245

tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc 882
 Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
 250 255 260

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930
 Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
 265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978
 Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
 285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026
 Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
 300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074
 Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
 315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122
 Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
 330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170
 Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
 345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
 Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
 365 370

gtgcccgcctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283
 tacttcccct ctctcttgtc cccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343
 ctctgtatg tacactgcag atacttccat ttggaccgc tgtggccaca gcatggcccc 1403
 tttagtcctc ccgccccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463
 tactcattgt tgcattgagc ctgtctgcca gccacccca gggactggg gcagcaccag 1523
 gtcccgggga gagggattga gccaagaggt gaggggtgcac gtcttcctc ctgtcccagc 1583
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 tggggacatg cggagtgggg gtcttatccc tgtgtgagc cctgagggca gagaggatgg 1703
 catgtttcag gggaggggga agccttctc tcaatttggt gtcagtga aa ttccaataaa 1763
 tgggatttgc tctctgcc 1781

<210> 43
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
 1 5 10 15
 Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
 20 25 30
 Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
 35 40 45
 Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
 50 55 60
 Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
 65 70 75 80
 Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
 85 90 95
 Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
 100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
 115 120 125
 Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
 130 135 140
 Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
 145 150 155 160
 Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
 165 170 175
 Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
 180 185 190
 Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
 195 200 205
 Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
 210 215 220
 Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
 225 230 235 240
 His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
 245 250 255
 Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
 260 265 270
 Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
 275 280 285
 Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
 290 295 300
 Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
 305 310 315 320
 Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
 325 330 335
 Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
 340 345 350
 His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
 355 360 365
 Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
 370 375 380
 Leu Val Pro Gly Pro Glu Lys Glu Asn
 385 390

<210> 44
 <211> 2396

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1228)

<400> 44
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Met Ser Asp
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gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
5 10 15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
20 25 30 35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
40 45 50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
55 60 65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
120 125 130

gac ccg gtg atg gtg ttg aac ccg tca ggg atg tgg cag gaa gag gtg 490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634

Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
 180 185 190 195
 atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
 Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
 200 205 210
 gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
 Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
 215 220 225
 gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
 Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
 230 235 240
 gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826
 Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
 245 250 255
 gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874
 Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
 260 265 270 275
 ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922
 Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
 280 285 290
 acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
 Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
 295 300 305
 cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018
 Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
 310 315 320
 tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066
 Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
 325 330 335
 ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
 Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
 340 345 350 355
 ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
 360 365 370
 aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
 375 380 385
 ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258
 Gly Pro Glu Lys Glu Asn
 390
 cagcgaaggg agaagttggg aagctacgtt ctgttgccca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct cctcccccg aagttctctg tggatgatgac cgctctcccc 1378
 tgccccctccc cgcttctctga cctctgaaga ggttggaag tgaccatttg gatgtctggg 1438
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 ccccgggcct gctgtgctgc tttgtgcca aggttagcca gtccccctg ttgtgttcca 1558
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 ctgccattct taaccaaggc agccccaagc ctctgggga ggcagggcaa aaacaggtgc 1858
 cctcatcgtg gtctgtgcca tgtcccgctc ctatgggtgt tgaggagaaa ggcggggaag 1918
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 gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038
 gaggccctac tgccttctca aagcagagag gcagcttata aaactcagcc caaaactctg 2098
 ttacatggg tggggagatg gagcaggaa gtacagagt ggatggtcag gacctgggcc 2158
 attgcaacca aaatggggac ttctgggta gggaggtcac tccctctact cactgagcta 2218
 ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278
 tcctcattgt ctaaagtagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338
 accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
 1 5 10 15
 Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
 20 25 30
 Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
 35 40 45
 Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
 50 55 60
 Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
 65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
 85 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
 100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
 115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
 130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
 145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
 165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
 180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
 195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
 210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
 225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
 245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
 260 265 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
 275 280 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
 290 295 300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
 305 310 315 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
 325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
 340 345 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
 355 360 365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
 370 375 380

Leu Val Pro Gly Pro Glu Lys Gln Asn
385 390

<210> 46
<211> 2396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1228)

<400> 46
agctgtgcac totccatcca gctgtgctgct ctgctcgga gtcccagcc atg tcc gac 58
Met Ser Asp
1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg	106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro	
5 10 15	
cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc	154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser	
20 25 30 35	
gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta	202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu	
40 45 50	
gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg	250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg	
55 60 65	
ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg	298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu	
70 75 80	
cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg	346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu	
85 90 95	
tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg	394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala	
100 105 110 115	
ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga	442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly	
120 125 130	
gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg	490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val	
135 140 145	
act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt	538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe	

150	155	160	
gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val 165 170 175			586
ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His 180 185 190 195			634
atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr 200 205 210			682
gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu 215 220 225			730
gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr 230 235 240			778
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile 245 250 255			826
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu 260 265 270 275			874
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu 280 285 290			922
acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn 295 300 305			970
cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val 310 315 320			1018
tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser 325 330 335			1066
ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys 340 345 350 355			1114
ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met 360 365 370			1162
aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro 375 380 385			1210

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac
 Gly Pro Glu Lys Gln Asn
 390

1258

cagcgaaggg agaagttggg aagctacgtt ctgttgcca ccagacttgc atttcagcct 1318
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 tcctcattgt ctaaagtgg cctaaatgtg tgaagtgcga tttctgctt tgtgtacccc 2338
 accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 47
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 47
 Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
 1 5 10 15

Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
 20 25 30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
50 55 60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
65 70 75 80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
115 120 125

Asp Lys Val Gly Glu Ser Asn Asn Met Val
130 135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(523)

<400> 48

agacgtggcg gctctcgccct gggctgtttc ccggcttcat ttctcccgac tcagcttccc 60

accctgggct ttccgaggtg ctgtcgccgc tgtccccacc actgcagcc atg atc tcc 118
Met Ile Ser
1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166
Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val
5 10 15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214
Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu
20 25 30 35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262
Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly
40 45 50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala
55 60 65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro
70 75 80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406
 Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg
 85 90 95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454
 Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
 100 105 110 115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502
 Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
 120 125 130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553
 Gly Glu Ser Asn Asn Met Val
 135

aaatattgtg ttatttataa agtcatttga agaattattca gcacaaaatt aaattacatg 613
 aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673
 caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733
 caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta 793
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 gtccactgca atggcaaaaa tatttccagt tgcactgtat ctctggaagt gatgcatgaa 973
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 ggattacttt tttttgtaaa catgggttaa ataaaacttc tgtgggttctt ctgaatotta 1093
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 aaagtctcat acttcttggg agtctgccct cctaagtatc tgtctatatc attcattacg 1273
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 tgtcatgatg taatttttct ttcttctttc ttttttttaa attttagcag tggcttatta 1453
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 attttcagct ttttcctagc atataatagt cattaagcat gacatatcct tcatatgatc 1633
 actcatcttg agttaattag aaaatacctg agttcacgtg ctaaagtcatt ttcactgtaa 1693
 taaactgact atgggtttctt aagaacatga cactaaaaaa aaagtgggtt ttttccaccg 1753
 ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

ttttagtggt gatgtaggga aacatttcaa cagccatagt actatttggt ttaccactga 1873
 ttgcactggt ttgttttttt aacagttgca aagcttttta atgcataaaa gtataattga 1933
 aatctgtggt atttattttac aaacatgtct acaaaaatag attacagctt attttatttt 1993
 tagttaaatc tcttaataca cagagaactc ccaatcttgc tcatctaaat aaggaaagac 2053
 ttggtgtata gtgtgatggt ttagtcttaa ggattaagac atttttggta cttgcatttg 2113
 acttacgatg tatctgtgaa aatgggatga tattgacaaa tggagactcc tacctcaata 2173
 gttaatggaa taataagagg ctactgttgt gtctaagtgt cttcaaaaaa gtaatatcct 2233
 cacttggaga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293
 actctgttac acatattttt gacctatatt atttacaatg tcttgataat tctacctttt 2353
 tagagcaaga atagtatctg ctaatgtaag ggacatctgt atttaactcc tttgtagaca 2413
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 aacatactag tctgctgata gaaagcacta tacatcctat tgtttctttc tttccaaaat 2713
 cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773
 catagcctta agtgtttctg tcattgttca agtgtatttt ctgtaacaga aacatatttg 2833
 gaatgttttt cttttcccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893
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 <211> 359
 <212> PRT
 <213> Homo sapiens

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 His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
 20 25 30
 Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
 35 40 45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
 50 55 60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
 65 70 75 80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
 85 90 95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser
 100 105 110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
 115 120 125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
 130 135 140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
 145 150 155 160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
 165 170 175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
 180 185 190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
 195 200 205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
 210 215 220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
 225 230 235 240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
 245 250 255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
 260 265 270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
 275 280 285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
 290 295 300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
 305 310 315 320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
 325 330 335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
 340 345 350

Arg Ser Thr Thr His Leu Ile
355

<210> 50
<211> 2636
<212> DNA
<213> Homo sapiens

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<222> (327)..(1403)

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aacgtggtgg acctatcctt gcaccagagg agattaagac tatttttgggt agcatcccag 180
atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240
atgagagcaa aagcattgggt gacatttttc tgaaatatc aaaagatttg gtaaaaacct 300
accctccctt tgtaaacctt tttgaa atg agc aag gaa aca att att aaa tgt 353
Met Ser Lys Glu Thr Ile Ile Lys Cys
1 5
gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401
Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala 25
10 15 20
aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449
Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro 40
30 35
gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497
Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys 55
45 50
cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545
His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile 70
60 65
gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593
Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys 85
75 80
aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641
Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly 105
90 95 100
tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689
Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val 120
110 115
gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737

Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val	
125	130 135
act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac	785
Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His	
140	145 150
aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca	833
Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro	
155	160 165
gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag	881
Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys	
170	175 180 185
gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg	929
Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu	
	190 195 200
ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag	977
Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln	
	205 210 215
atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt	1025
Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys	
	220 225 230
cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att	1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile	
	235 240 245
tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac	1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp	
250	255 260 265
agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag	1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys	
	270 275 280
gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga	1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg	
	285 290 295
agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc	1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser	
	300 305 310
agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta	1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu	
	315 320 325
gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa	1361
Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu	
330	335 340 345
agg aga agt cat acg tta agt aga tct aca act cat ttg ata	1403
Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile	

tgaagcgtta ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463
 aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523
 cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583
 caagttaatt catgtaaaaa atgatagtga ttttgatgta atttatctct tgtttgaatc 1643
 tgtcattcaa aggccaataa ttttaagttgc tatcagctga tattagtagc tttgcaaccc 1703
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 gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823
 aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883
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 aagcgttttc aagatctagc atgtggattt taaaagattt gccctcatta acaagaataa 2003
 catttaaagg agattgtttc aaaatatattt tgcaaattga gataaggaca gaaagattga 2063
 gaaacattgt atattttgca aaaacaagat gttttagct gtttcagaga gagtacggta 2123
 tatttatggg aattttatcc actagcaa attgatttag tttgatagtg tgtggaattt 2183
 tattttgaag gataagacca tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa 2243
 ataattctga agttgccatc agttttacta atcttctgtg aaatgcatag atatgogcat 2303
 gttcaacttt ttattgtggg cttataatta aatgtaaaat tgaaaattca tttgctgttt 2363
 caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423
 catatggata aatgcatttt tatttcctat ttctttaggg agtgctacaa atgtttgtca 2483
 cttaaatttc aagtttctgt tttaatagtt aactgactat agattgttt ctatgccatg 2543
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 agtaagaact ttgtaaataa atacctaaaa ccc 2636

<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

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Ala	Asp	Ser	Ser	Ile	Phe	Asp	Ser	Lys	Val	Thr	Glu	Ile	Ser	Lys	Glu
				20				25					30		

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
 35 40 45
 Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
 50 55 60
 Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
 65 70 75 80
 Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
 85 90 95
 Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
 100 105 110
 Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
 115 120 125
 Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
 130 135 140
 Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
 145 150 155 160
 Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
 165 170 175
 Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
 180 185 190
 Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
 195 200 205
 Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
 210 215 220
 Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
 225 230 235 240
 Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
 245 250 255
 Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu
 260 265 270
 Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys
 275 280 285
 Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu
 290 295 300
 Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
 305 310 315 320
 Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
 325 330 335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
 340 345 350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
 355 360 365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
 370 375 380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
 385 390 395 400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
 405 410 415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
 420 425 430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
 435 440 445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
 450 455 460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
 465 470 475 480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
 485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
 500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
 515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
 530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
 545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu
 565 570 575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
 580 585 590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
 595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
 610 615 620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
 625 630 635 640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
 645 650 655
 Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
 660 665 670
 Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
 675 680 685
 Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
 690 695 700
 Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
 705 710 715 720
 Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val
 725 730 735
 Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp
 740 745 750
 Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp
 755 760 765
 Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
 770 775 780
 Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
 785 790 795 800
 Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
 805 810 815
 Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu
 820 825 830
 Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
 835 840 845
 Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
 850 855 860
 Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr
 865 870 875 880
 His Leu Ile

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 <211> 3910
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 <213> Homo sapiens

<220>
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 <222> (29)..(2677)

<400> 52

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1 5

tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct 100
Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser
10 15 20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca 148
Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser
25 30 35 40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196
Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val
45 50 55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile
60 65 70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292
Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu
75 80 85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat 340
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp
90 95 100

tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca 388
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro
105 110 115 120

cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca 436
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser
125 130 135

tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt 484
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe
140 145 150

act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc 532
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val
155 160 165

cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca 580
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr
170 175 180

cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg 628
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val
185 190 195 200

agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg 676
Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
205 210 215

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga	724
Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg	
220 225 230	
aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg	772
Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu	
235 240 245	
gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg	820
Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met	
250 255 260	
caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt	868
Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu	
265 270 275 280	
gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag	916
Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys	
285 290 295	
aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg	964
Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met	
300 305 310	
gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act	1012
Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr	
315 320 325	
cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac	1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn	
330 335 340	
agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca	1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser	
345 350 355 360	
aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct	1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala	
365 370 375	
gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca	1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro	
380 385 390	
gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct	1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser	
395 400 405	
tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa	1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln	
410 415 420	
gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg	1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu	
425 430 435 440	

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa	1396
Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln	
445 450 455	
cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt	1444
Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly	
460 465 470	
agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt	1492
Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu	
475 480 485	
gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att	1540
Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile	
490 495 500	
ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta	1588
Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val	
505 510 515 520	
aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag	1636
Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln	
525 530 535	
aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa	1684
Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu	
540 545 550	
tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg	1732
Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg	
555 560 565	
tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct	1780
Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala	
570 575 580	
gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg	1828
Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu	
585 590 595 600	
aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct	1876
Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala	
605 610 615	
caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct	1924
Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala	
620 625 630	
aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att	1972
Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile	
635 640 645	
tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc	2020
Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe	
650 655 660	
ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att	2068

Leu Phe Asn Asp Cys	Leu Glu Ile Ala Arg	Lys Arg His Lys Val Ile	
665	670	675	680
ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt			2116
Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu			
	685	690	695
aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac			2164
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp			
	700	705	710
ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg			2212
Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg			
	715	720	725
cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca			2260
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser			
	730	735	740
gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta			2308
Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val			
	745	750	755
gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct			2356
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala			
	765	770	775
gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg			2404
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu			
	780	785	790
agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga			2452
Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg			
	795	800	805
gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt			2500
Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu			
	810	815	820
atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat			2548
Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp			
	825	830	835
aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc			2596
Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile			
	845	850	855
cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt			2644
Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser			
	860	865	870
cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt			2697
His Thr Leu Ser Arg Ser Thr Thr His Leu Ile			
	875	880	
aaattataga aatgtataga cacctcatatc tcaaataaga aactgactta aatgggtactt			2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817
 tttttcttct tgaaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa 2877
 atgatagtga ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937
 ttttaagttgc tatcagctga tattagtagc tttgcaaccc tgatagagta aataaatttt 2997
 atgggcggggt gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057
 ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117
 tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177
 tatttaaata accactcctt tcacagttaa ttttcttctc aagcgttttc aagatctagc 3237
 atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297
 aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357
 aaaacaagat gttttagct gtttcagaga gactacggta ttttatggt aattttatcc 3417
 actagcaaat cttgatthag tttgatagtg tgtggaattt tttttgaag gataagacca 3477
 tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa ataattctga agttgccatc 3537
 agttttacta atcttctgtg aaatgcatag atatgcgcac gttcaacttt ttattgtggt 3597
 cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657
 aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717
 tatttcctat ttctttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777
 tttaatagtt aactgactat agattgtttt ctatgccatg tatgtgccac ttctgagagt 3837
 agtaaatac tctttgctac attttaaag caattgtatt agtaagaact ttgtaaataa 3897
 atacctaaaa ccc 3910

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 <211> 622
 <212> PRT
 <213> Homo sapiens

<400> 53
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 Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn
 20 25 30
 Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser
 35 40 45
 Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg

50

55

60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
 65 70 75 80
 Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
 85 90 95
 Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly
 100 105 110
 Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
 115 120 125
 Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
 130 135 140
 Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
 145 150 155 160
 His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
 165 170 175
 Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
 180 185 190
 Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
 195 200 205
 Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
 210 215 220
 Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly
 225 230 235 240
 Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met
 245 250 255
 Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
 260 265 270
 Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln
 275 280 285
 Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp
 290 295 300
 Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
 305 310 315 320
 Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg
 325 330 335
 Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu
 340 345 350
 Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe

355	360	365
Pro Asp Leu Ala Gly Ala	Pro Phe Tyr Phe Ser	Phe Ile Phe Ser Ile
370	375	380
Val Ala Phe Leu Tyr Phe	Phe Tyr Lys Thr Trp	Ala Thr Asp Pro Gly
385	390	395 400
Phe Thr Lys Ala Ser Glu	Glu Glu Lys Lys Val	Asn Ile Ile Thr Leu
405	410	415
Ala Glu Thr Gly Ser Leu	Asp Phe Arg Thr Phe	Cys Thr Ser Cys Leu
420	425	430
Ile Arg Lys Pro Leu Arg	Ser Leu His Cys His	Val Cys Asn Cys Cys
435	440	445
Val Ala Arg Tyr Asp Gln	His Cys Leu Trp Thr	Gly Arg Cys Ile Gly
450	455	460
Phe Gly Asn His His Tyr	Tyr Ile Phe Phe Leu	Phe Phe Leu Ser Met
465	470	475 480
Val Cys Gly Trp Ile Ile	Tyr Gly Ser Phe Ile	Tyr Leu Ser Ser His
485	490	495
Cys Ala Thr Thr Phe Lys	Glu Asp Gly Leu Trp	Thr Tyr Leu Asn Gln
500	505	510
Ile Val Ala Cys Ser Pro	Trp Val Leu Tyr Ile	Leu Met Leu Ala Thr
515	520	525
Phe His Phe Ser Trp Ser	Thr Phe Leu Leu Leu	Asn Gln Leu Phe Gln
530	535	540
Ile Ala Phe Leu Gly Leu	Thr Ser His Glu Arg	Ile Ser Leu Gln Lys
545	550	555 560
Gln Ser Lys His Met Lys	Gln Thr Leu Ser Leu	Arg Lys Thr Pro Tyr
565	570	575
Asn Leu Gly Phe Met Gln	Asn Leu Ala Asp Phe	Phe Gln Cys Gly Cys
580	585	590
Phe Gly Leu Val Lys Pro	Cys Val Val Asp Trp	Thr Ser Gln Tyr Thr
595	600	605
Met Val Phe His Pro Ala	Arg Glu Lys Val Leu	Arg Ser Val
610	615	620

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<221> CDS

<222> (104)..(1969)

<400> 54

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115
Met Glu Gly Pro
1

ggg ctg ggc tgc cag tgc agg aat cac agc cat ggc ccc cac cct cca 163
Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro
5 10 15 20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211
Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala
25 30 35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259
Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp
40 45 50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307
Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu
55 60 65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tgc 355
Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser
70 75 80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403
Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
85 90 95 100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451
Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
105 110 115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499
Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
120 125 130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547
Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
135 140 145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595
Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
150 155 160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643
Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val
165 170 175 180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691
Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro
185 190 195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val 200 205 210	739
gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly 215 220 225	787
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp 230 235 240	835
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn 245 250 255 260	883
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg 265 270 275	931
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu 280 285 290	979
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr 295 300 305	1027
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu 310 315 320	1075
gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly 325 330 335 340	1123
tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val 345 350 355	1171
ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala 360 365 370	1219
gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu 375 380 385	1267
tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala 390 395 400	1315
tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly 405 410 415 420	1363

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca	1411
Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro	
425 430 435	
tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat	1459
Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr	
440 445 450	
gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat	1507
Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His	
455 460 465	
cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg	1555
His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp	
470 475 480	
att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca	1603
Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr	
485 490 495 500	
ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt	1651
Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys	
505 510 515	
tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca	1699
Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser	
520 525 530	
tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg	1747
Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu	
535 540 545	
ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat	1795
Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His	
550 555 560	
atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc	1843
Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe	
565 570 575 580	
atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg	1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val	
585 590 595	
aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac	1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His	
600 605 610	
cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa	1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val	
615 620	
ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaaag tgaagtaaaag	2049
atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa	2109
aagttctcaa taaaggcatt acaatttttt aggttttagaa agatggactt ttctgataaa	2169

ttttggcaga catctaaaaa aaaaaccata tttttcacaa gaaaatgcaa gttacttttt 2229
 ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct 2289
 gtttcaaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg 2349
 tatctataaa tatgtaaaaa atattttaaat agatgtacct gttttgcttt cacacttaat 2409
 aaaaaatttt tttttgt 2426

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 <212> PRT
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<400> 55
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 20 25 30
 Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
 35 40 45
 Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
 50 55 60
 Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65 70 75 80
 Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
 85 90 95
 Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly
 115 120 125
 Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly
 130 135 140
 Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln
 145 150 155 160
 His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly
 165 170 175
 Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu
 180 185 190
 Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala
 195 200 205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
 210 215 220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
 225 230 235 240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
 245 250 255

Gly

<210> 56
 <211> 1520
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (10)..(780)

<400> 56
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 1 5 10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99
 Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly
 15 20 25 30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147
 Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg
 35 40 45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195
 Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
 50 55 60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243
 Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
 65 70 75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291
 Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
 80 85 90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339
 Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95 100 105 110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387
 Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
 115 120 125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435
 Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser

130

135

140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483
 Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser
 145 150 155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531
 Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro
 160 165 170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579
 Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
 175 180 185 190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627
 Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
 195 200 205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675
 Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
 210 215 220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723
 Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
 225 230 235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771
 Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
 240 245 250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820
 Thr Asp Gly
 255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttatatt atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tctgtttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttgaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg ccaggaagg gcacaggggc tgagcactac agaagtcaca tgggtttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag 1520

<210> 57
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 57
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 20 25 30
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 35 40 45
 Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
 50 55 60
 Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
 65 70 75 80
 Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
 85 90 95
 Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
 100 105

<210> 58
 <211> 1496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (9)..(329)

<400> 58
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 Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
 1 5 10
 atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98
 Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
 15 20 25 30
 gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146
 Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
 35 40 45
 gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194
 Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
 50 55 60
 cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242

Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp
65 70 75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290
Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met
80 85 90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339
Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
95 100 105

tttgatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399
ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459
caaaccattc agatcagcca cttgctgacc ctggttctta aggacacatg acattagtcc 519
aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccca ggactcagtc 579
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ataaaacatg ttgtaat 1496

<210> 59
<211> 272
<212> PRT
<213> Homo sapiens

<400> 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly
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Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp
20 25 30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met
35 40 45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
50 55 60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
65 70 75 80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
85 90 95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
100 105 110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
115 120 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
130 135 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
145 150 155 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro
165 170 175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val
180 185 190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr
195 200 205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu
210 215 220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln
225 230 235 240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu
245 250 255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
260 265 270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117)..(932)

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gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggctctgcc tcagcc atg 119
Met
1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167
Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro
5 10 15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215
Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val
20 25 30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263
Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met
35 40 45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311
Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile
50 55 60 65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359
Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly
70 75 80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407
Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu
85 90 95

ggc gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455
Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr
100 105 110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503
Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val
115 120 125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551
Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599
Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647
Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu
 180 185 190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743
 Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr
 195 200 205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791
 Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met
 210 215 220 225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839
 His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr
 230 235 240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887
 Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg
 245 250 255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932
 Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
 260 265 270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992
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 taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgactg 1112
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 gaaattagtc tcatagtga gtgaacttca accccaaaat tttaaaaatg tatttcccc 1472
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 ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772
 tctgaaaatt ttattagttt attcttggtg agaataccaa gaaaatgtgt atttgcccat 1832
 tgctaaatat gatatatgcc attttgtatt tatttgctcc aagtgtcttt ttttaagagg 1892
 agaataaaca ataaggaatt actg 1916

<210> 61
<211> 219
<212> PRT
<213> Homo sapiens

<400> 61
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Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp
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Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
35 40 45
Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
50 55 60
Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
65 70 75 80
Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
85 90 95
Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
100 105 110
Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
115 120 125
Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
130 135 140
Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
145 150 155 160
Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
165 170 175
Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
180 185 190
Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
195 200 205
Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
210 215

<210> 62
<211> 1362
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (49)..(705)

<400> 62

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                                     Met Asn Arg
                                     1

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105
Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp
      5                      10                      15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153
Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile
      20                      25                      30                      35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys
      40                      45                      50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg
      55                      60                      65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala
      70                      75                      80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu
      85                      90                      95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu
     100                      105                      110                      115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu
      120                      125                      130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu
      135                      140                      145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu
      150                      155                      160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
      165                      170                      175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
     180                      185                      190                      195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681
Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
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gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735
 Gly Leu Pro Gln Ile Pro Ala Ser
 215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat 795
 ttaggtttct ttcttttctt tgaaggaaag ttttaattaca ttgctctttt attttttcca 855
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 tatactcaat aaatattttt caaaagg 1362

<210> 63

<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

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Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly
 20 25 30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr
 35 40 45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg
 50 55 60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn
 65 70 75 80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val
 85 90 95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp
 100 105 110

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser

115	120	125
Met Val Val Gln Leu Met	Lys Tyr Gly Ala Asp	Pro Ser Leu Ile Asp
130	135	140
Gly Glu Gly Cys Ser Cys	Ile His Leu Ala Ala	Gln Phe Gly His Thr
145	150	155
Ser Ile Val Ala Tyr Leu	Ile Ala Lys Gly Gln	Asp Val Asp Met Met
165	170	175
Asp Gln Asn Gly Met Thr	Pro Leu Met Trp Ala	Ala Tyr Arg Thr His
180	185	190
Ser Val Asp Pro Thr Arg	Leu Leu Leu Thr Phe	Asn Val Ser Val Asn
195	200	205
Leu Gly Asp Lys Tyr His	Lys Asn Thr Ala Leu	His Trp Ala Val Leu
210	215	220
Ala Gly Asn Thr Thr Val	Ile Ser Leu Leu Leu	Glu Ala Gly Ala Asn
225	230	235
Val Asp Ala Gln Asn Ile	Lys Gly Glu Ser Ala	Leu Asp Leu Ala Lys
245	250	255
Gln Arg Lys Asn Val Trp	Met Ile Asn His Leu	Gln Glu Ala Arg Gln
260	265	270
Ala Lys Gly Tyr Asp Asn	Pro Ser Phe Leu Arg	Lys Leu Lys Ala Asp
275	280	285
Lys Glu Phe Arg Gln Lys	Val Met Leu Gly Thr	Pro Phe Leu Val Ile
290	295	300
Trp Leu Val Gly Phe Ile	Ala Asp Leu Asn Ile	Asp Ser Trp Leu Ile
305	310	315
Lys Gly Leu Met Tyr Gly	Gly Val Trp Ala Thr	Val Gln Phe Leu Ser
325	330	335
Lys Ser Phe Phe Asp His	Ser Met His Ser Ala	Leu Pro Leu Gly Ile
340	345	350
Tyr Leu Ala Thr Lys Phe	Trp Met Tyr Val Thr	Trp Phe Phe Trp Phe
355	360	365
Trp Asn Asp Leu Asn Phe	Leu Phe Ile His Leu	Pro Phe Leu Ala Asn
370	375	380
Ser Val Ala Leu Phe Tyr	Asn Phe Gly Lys Ser	Trp Lys Ser Asp Pro
385	390	395
Gly Ile Ile Lys Ala Thr	Glu Glu Gln Lys Lys	Lys Thr Ile Val Glu
405	410	415
Leu Ala Glu Thr Gly Ser	Leu Asp Leu Ser Ile	Phe Cys Ser Thr Cys

420

425

430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
 435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
 450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
 465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
 485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
 500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
 515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
 530 535 540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
 545 550 555 560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
 565 570 575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
 580 585 590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
 595 600 605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
 610 615 620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1879)

<400> 64

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ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97
 Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
 15 20 25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat	145
Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp	
30 35 40	
gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat	193
Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr	
45 50 55 60	
gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg	241
Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro	
65 70 75	
gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga	289
Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg	
80 85 90	
ata gat tta gtc aaa tac tat att tgc aaa ggt gct att gtg gat caa	337
Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln	
95 100 105	
ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa	385
Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln	
110 115 120	
ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct	433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro	
125 130 135 140	
tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag	481
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln	
145 150 155	
ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat	529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp	
160 165 170	
gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca	577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala	
175 180 185	
tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat	625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn	
190 195 200	
gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat	673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His	
205 210 215 220	
tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa	721
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu	
225 230 235	
gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt	769
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu	
240 245 250	
gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa	817

Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln	
255	260 265
gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag	865
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys	
270	275 280
ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct	913
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro	
285	290 295 300
ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat	961
Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp	
	305 310 315
tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta	1009
Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val	
	320 325 330
cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg	1057
Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu	
	335 340 345
ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg	1105
Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp	
	350 355 360
ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca	1153
Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro	
	365 370 375 380
ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg	1201
Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp	
	385 390 395
aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag	1249
Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys	
	400 405 410
aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc	1297
Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe	
	415 420 425
tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt	1345
Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly	
	430 435 440
gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg	1393
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val	
	445 450 455 460
ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta	1441
Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu	
	465 470 475
ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct	1489
Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser	

480

485

490

tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg 1537
 Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp
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aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg 1585
 Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met
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 Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met
 525 530 535 540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681
 Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg
 545 550 555

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 Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile
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 Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe
 575 580 585

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 Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr
 590 595 600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag 1873
 Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln
 605 610 615 620

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 Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

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cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtac 2289

gagtattgca tctaattcca ggagcattgt ttttaagttga ttgactagtt attatgtaca 2349

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 cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709
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 aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889
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 <213> Homo sapiens

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 Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly
 35 40 45
 Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala
 50 55 60
 Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly
 65 70 75 80
 Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp
 85 90 95
 Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys
 100 105 110
 Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu
 115 120 125
 His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met
 130 135 140
 Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys
 145 150 155 160
 Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu
 165 170 175
 Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr
 180 185 190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg
 195 200 205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His
 210 215 220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val
 225 230 235 240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile
 245 250 255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp
 260 265 270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn
 275 280 285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys
 290 295 300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
 305 310 315 320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly
 325 330 335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His
 340 345 350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe
 355 360 365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
 370 375 380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr
 385 390 395 400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr
 405 410 415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser
 420 425 430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val
 435 440 445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp
 450 455 460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg
 465 470 475 480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met
 485 490 495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr
 500 505 510
 Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser
 515 520 525
 Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp
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 Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly
 545 550 555 560
 Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys
 565 570 575
 Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg
 580 585 590
 Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro
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 Ser Gly Ser Gly Tyr Gln Leu Val
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 Met Gln Arg
 1
 gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164
 Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp
 5 10 15
 acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212
 Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro
 20 25 30 35
 caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260
 Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr
 40 45 50
 cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308

His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr
55 60 65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356
Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val
70 75 80

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404
Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile
85 90 95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452
Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile
100 105 110 115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500
Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala
120 125 130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly
135 140 145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596
Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu
150 155 160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644
Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys
165 170 175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692
Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met
180 185 190 195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740
Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu
200 205 210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788
Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr
215 220 225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836
Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu
230 235 240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884
Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu
245 250 255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932
Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn
260 265 270 275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980
His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe

280

285

290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta 1028
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 295 300 305

gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta 1076
 Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu
 310 315 320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg 1124
 Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp
 325 330 335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat 1172
 Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His
 340 345 350 355

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 Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr
 360 365 370

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 Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile
 375 380 385

cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga 1316
 His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly
 390 395 400

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa 1364
 Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln
 405 410 415

aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc 1412
 Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu
 420 425 430 435

agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa 1460
 Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys
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cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc 1508
 His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys
 455 460 465

cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg 1556
 Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met
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 Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly
 485 490 495

tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat 1652
 Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp
 500 505 510 515

gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700
 Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met
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 Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val
 535 540 545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796
 Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr
 550 555 560

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 565 570 575

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 Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val
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 Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser
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 Gly Tyr Gln Leu Val
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 35 40 45
 Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
 50 55 60
 Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
 65 70 75 80
 Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
 85 90 95
 Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
 100 105 110
 Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
 115 120 125
 Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
 130 135 140
 Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
 145 150 155 160
 Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
 165 170 175
 Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
 180 185 190
 Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
 195 200 205
 Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
 210 215 220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
 225 230 235 240
 Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
 245 250 255
 Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
 260 265 270
 His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
 275 280 285
 Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
 290 295 300
 Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
 305 310 315 320
 Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
 325 330 335
 Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
 340 345 350
 Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
 355 360 365
 Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
 370 375 380
 Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
 385 390 395 400
 Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
 405 410 415
 Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
 420 425 430
 Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
 435 440 445
 Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
 450 455 460
 Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
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 Ser Cys

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His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His															25
15 20															
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Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val															55
45 50															
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His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly															70
60 65															
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Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu															90
75 80 85															
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Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro															105
95 100															
gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg															387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg															120
110 115															
act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag															435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu															135
125 130 135															
cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc															483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly															150
140 145															
ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac															531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn															170
155 160 165															
tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag															579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln															185
175 180															

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val 190 195 200	627
acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val 205 210 215	675
cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro 220 225 230	723
ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu 235 240 245 250	771
gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala 255 260 265	819
cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys 270 275 280	867
ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp 285 290 295	915
ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro 300 305 310	963
gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu 315 320 325 330	1011
aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly 335 340 345	1059
tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr 350 355 360	1107
cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser 365 370 375	1155
tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly 380 385 390	1203
act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp 395 400 405 410	1251
ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc	1299

Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
 415 420 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
 Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
 430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395
 Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu
 445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
 Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
 460 465 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
 Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
 475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545
 Gln Lys Leu Trp Glu Phe Ser Cys
 495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcagggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg 1845

atttcctagg agttgggttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
 1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
 20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
 35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
 50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
 65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
 85 90 95
 Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
 100 105 110
 Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
 115 120 125
 Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
 130 135 140
 Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
 145 150 155 160
 Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
 165 170 175
 Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
 180 185 190
 Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
 195 200 205
 Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
 210 215 220
 Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
 225 230 235 240
 Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
 245 250 255
 Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
 260 265 270
 His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
 275 280 285
 Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
 290 295 300
 Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
 305 310 315 320
 Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
 325 330 335
 Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
 340 345 350
 Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
 355 360 365
 Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
 370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
435 440 445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
485 490 495

Ser Cys

<210> 70
<211> 1902
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (22)..(1515)

<400> 70
gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51
Met Ala Arg Leu Glu Val Ile Glu Leu Pro 10
1 5

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His 25
15 20

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile 40
30 35

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val 55
45 50

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly 70
60 65

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75

80

85

90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct	339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro	
95 100 105	
gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg	387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg	
110 115 120	
act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag	435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu	
125 130 135	
cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc	483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly	
140 145 150	
ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac	531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn	
155 160 165 170	
tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag	579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln	
175 180 185	
gtg gcg gcg tac aac ggg gcc ggt ctg gcc gtc ttc agc agg gca gtg	627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val	
190 195 200	
acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg	675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val	
205 210 215	
cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct	723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro	
220 225 230	
ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg	771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu	
235 240 245 250	
gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc	819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala	
255 260 265	
cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag	867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys	
270 275 280	
ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac	915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp	
285 290 295	
ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca	963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro	
300 305 310	

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011
 Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
 315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059
 Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
 335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107
 Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
 350 355 360

cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca 1155
 His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser
 365 370 375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203
 Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
 380 385 390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251
 Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
 395 400 405 410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299
 Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
 415 420 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
 Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
 430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta 1395
 Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu
 445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
 Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
 460 465 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
 Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
 475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545
 Gln Lys Leu Trp Glu Phe Ser Cys
 495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttcttttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcagggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845
 atttctagg agttgggttt ttttttttta aagcataaat aaatttaatt gcacag 1902

<210> 71
 <211> 245
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
 1 5 10 15
 Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
 20 25 30
 Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
 35 40 45
 Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
 50 55 60
 Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
 65 70 75 80
 Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
 85 90 95
 Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
 100 105 110
 Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
 115 120 125
 Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
 130 135 140
 Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
 145 150 155 160
 Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
 165 170 175
 Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
 180 185 190
 Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
 195 200 205
 Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
 210 215 220
 Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
 225 230 235 240
 Gln Trp Ile Gln Arg

<210> 72
 <211> 1551
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (127)..(861)

<400> 72
 ggaagtcggc caccttcctc cgtcccgcc gttagcccag ccaagcccag ccaagcccag 60
 ccaagcccag ccgatcgcg gcaccggagc cagccccgca gcgggtccc cctgtctgtc 120
 acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168
 Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser
 1 5 10
 atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216
 Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser
 15 20 25 30
 atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264
 Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile
 35 40 45
 ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312
 Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His
 50 55 60
 cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360
 Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg
 65 70 75
 ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408
 Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser
 80 85 90
 ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456
 Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile
 95 100 105 110
 gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504
 Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe
 115 120 125
 agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552
 Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys
 130 135 140
 gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600
 Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu
 145 150 155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648
 Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn
 160 165 170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696
 Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile
 175 180 185 190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744
 Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly
 195 200 205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792
 Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
 210 215 220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt 840
 Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val
 225 230 235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact 891
 Leu Gly Gln Trp Ile Gln Arg
 240 245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951
 ctagggtctg tgaacgaggc ctgtctcttc cctgggggttt ctttccatgg cttttatttc 1011
 tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggtctg 1071
 ggctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagaccagc 1131
 tagtgaggga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191
 tcaccgggca tagcctggaa gcccgaagtc tgttctgact ttgcctggct gtctccttga 1251
 cccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311
 tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371
 tcagcacctg agtcacagcc cagggtgccg gaagcagcct ctgcgcatag gcagtgattt 1431
 gcgattactt taaagctcac cttttttctt cccctctctg ttgcgtctg tcagcataat 1491
 gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgagggag 1551

<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
 1 5 10 15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20

25

30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
195 200 205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
210 215 220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225 230 235 240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
245 250 255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
290 295 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
 340 345 350

<210> 74
 <211> 2401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (103)..(1158)

<400> 74
 ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60
 tacccttggc gccacagtcg gccaccgggg ctgcgcgcgcg tc atg gag agc gga 114
 Met Glu Ser Gly
 1
 ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162
 Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
 5 10 15 20
 gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210
 Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
 25 30 35
 caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258
 Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
 40 45 50
 agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306
 Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
 55 60 65
 gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354
 Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
 70 75 80
 gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402
 Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
 85 90 95 100
 atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
 Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
 105 110 115
 att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
 Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
 120 125 130
 gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546
 Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
 135 140 145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag	594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln	
150 155 160	
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Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys	
165 170 175 180	
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca	690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr	
185 190 195	
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Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro	
200 205 210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc	786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser	
215 220 225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg	834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala	
230 235 240	
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg	882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg	
245 250 255 260	
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag	930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln	
265 270 275	
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct	978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro	
280 285 290	
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc	1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser	
295 300 305	
ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc	1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr	
310 315 320	
gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga	1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg	
325 330 335 340	
cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg	1168
Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser	
345 350	
gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga	1228
ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa	1288

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 tcgcttctcc ttgtgttacc ccctcccagt attaccattt gccctcacc tgcccttggg 2188
 gagcctttta gtgcaagaca gatggggctg ttttcccca cctctgagta gttggaggtc 2248
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 <212> PRT
 <213> Homo sapiens

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 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
 35 40 45
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
 50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
 65 70 75 80
 Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
 85 90 95
 Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
 100 105 110
 Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
 115 120 125
 Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
 130 135 140
 Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
 145 150 155 160
 Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
 165 170 175
 Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
 180 185 190
 Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
 195 200 205
 Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
 210 215 220
 Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
 225 230 235 240
 Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
 245 250 255
 Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
 260 265 270
 Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
 275 280 285
 Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
 290 295 300
 Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
 305 310 315 320
 Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
 325 330 335
 Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
 340 345 350

<210> 76
 <211> 2401

<212> DNA
<213> Homo sapiens

<220>
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<400> 76

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                                   Met Glu Ser Gly
                                   1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg      162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
  5                      10                      15                      20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc      210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
                      25                      30                      35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag      258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
                      40                      45                      50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata      306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
                      55                      60                      65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg      354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
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gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag      402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
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atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc      450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
                      105                      110                      115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag      498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
                      120                      125                      130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg      546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
                      135                      140                      145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag      594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
                      150                      155                      160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa      642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165                      170                      175                      180
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Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr	
185 190 195	
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg	738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro	
200 205 210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc	786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser	
215 220 225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg	834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala	
230 235 240	
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg	882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg	
245 250 255 260	
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag	930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln	
265 270 275	
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct	978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro	
280 285 290	
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc	1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser	
295 300 305	
ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc	1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr	
310 315 320	
gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga	1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg	
325 330 335 340	
cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg	1168
Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser	
345 350	
gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga	1228
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tcgggtagaa actctccaga cccatgcctc caatggcagg atgtctgcctt tcccacctga	1348
gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg	1408
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caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tggttttttc tggatgaatcg	1528

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<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

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Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile
 35 40 45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile
 50 55 60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile
 65 70 75 80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
 85 90 95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser
 100 105 110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
 115 120 125
 Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
 130 135 140
 Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
 145 150 155 160
 Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
 165 170 175
 Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
 180 185 190
 Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
 195 200 205
 Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
 210 215 220
 Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
 225 230 235 240
 Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
 245 250 255
 Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
 260 265 270
 Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
 275 280 285
 His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
 290 295 300
 Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
 305 310 315 320
 Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp
 325 330 335
 Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe
 340 345 350
 Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
 355 360 365
 Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
 370 375 380
 Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
 385 390 395 400
 His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
 405 410 415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu
 420 425 430
 Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
 435 440 445
 Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
 450 455 460
 Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
 465 470 475 480
 Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
 485 490 495
 Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
 500 505 510
 Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
 515 520 525
 Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
 530 535 540
 Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
 545 550 555 560
 Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
 565 570 575
 Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
 580 585 590
 Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
 595 600 605
 Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
 610 615 620
 Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met
 625 630 635 640
 Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
 645 650 655
 Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
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<210> 78

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 ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240
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 ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgaggga aaagcccaca 360
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 Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu
 1 5 10
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 Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
 15 20 25
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 His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu
 30 35 40 45
 gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554
 Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
 50 55 60
 tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602
 Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile
 65 70 75
 gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650
 Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser
 80 85 90
 ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698
 Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu
 95 100 105
 gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746
 Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
 110 115 120 125
 ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794
 Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu
 130 135 140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt	842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val	
145 150 155	
gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg	890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu	
160 165 170	
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Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met	
175 180 185	
ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta	986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu	
190 195 200 205	
gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa	1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys	
210 215 220	
aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct	1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro	
225 230 235	
ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa	1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys	
240 245 250	
ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt	1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe	
255 260 265	
gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt	1226
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu	
270 275 280 285	
aga gac act cac ctg tgg tat ttt gta ata cct ggc ttt tcc att ttt	1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe	
290 295 300	
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Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp	
305 310 315	
gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac	1370
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His	
320 325 330	
agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg	1418
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met	
335 340 345	
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Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu	
350 355 360 365	
gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att	1514

Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile	
370 375 380	
ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat	1562
Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His	
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Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly	
400 405 410	
tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca	1658
Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro	
415 420 425	
aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act	1706
Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr	
430 435 440 445	
ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag	1754
Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu	
450 455 460	
acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg	1802
Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu	
465 470 475	
cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc	1850
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro	
480 485 490	
aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca	1898
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr	
495 500 505	
gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt	1946
Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu	
510 515 520 525	
ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att	1994
Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile	
530 535 540	
atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg	2042
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg	
545 550 555	
aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa	2090
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys	
560 565 570	
aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca	2138
Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr	
575 580 585	
aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg	2186
Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp	

590

595

600

605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234
 Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
 610 615 620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282
 Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
 625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330
 His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
 640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378
 Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
 655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426
 Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
 670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac 2472
 Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
 690 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532
 gtatgctgta tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg 2592
 tctttttctta agtaattatg gtatatataa ggcgttgggga aaaaacattt tataatgaaa 2652
 gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712
 ctttcaggaa tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa 2772
 tgggtcaatga tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat 2832
 gtagaccaga taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt 2892
 cttttttcca aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct 2952
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<210> 79

<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

Met Glu Ala Ala Ser Leu Ser Leu Ser Asn Leu Trp Phe Gly Phe Leu
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Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val
 20 25 30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg
 35 40 45
 Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg
 50 55 60
 Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala
 65 70 75 80
 Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu
 85 90 95
 Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser
 100 105 110
 Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe
 115 120 125
 Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
 130 135 140
 Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
 145 150 155 160
 Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
 165 170 175
 Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
 180 185 190
 Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
 195 200 205
 Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
 210 215 220
 Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
 225 230 235 240
 His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
 245 250 255
 Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
 260 265 270
 Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
 275 280 285
 Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
 290 295 300
 Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
 305 310 315 320
 Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe
 325 330 335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
 340 345 350
 Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe
 355 360 365
 Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser
 370 375 380
 Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu
 385 390 395 400
 Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr
 405 410 415
 Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp
 420 425 430
 Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly
 435 440 445
 Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr
 450 455 460
 Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val
 465 470 475 480
 Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro
 485 490 495
 Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
 500 505 510
 Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
 515 520 525
 Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro
 530 535 540
 Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile
 545 550 555 560
 Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu
 565 570 575
 Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met
 580 585 590
 Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu
 595 600 605
 Val Lys Ser
 610

<210> 80
 <211> 3007

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (629)..(2461)

<400> 80
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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120
ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180
ggtttggttt tggaactgac tccgaggggtt gggagagcgc gttggtggcg acggccgagt 240
cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300
ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360
ttgctggtta catgtgtaaa tcaactgcgtt attgctttag tcattgtctc tatttagcaa 420
tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggatatctg 480
ctattttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540
aaaaacagca aattccttaa ttttgtaat ttttattctt ggtctttttg ttcttggaat 600
cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652
Met Glu Ala Ala Ser Leu Ser Leu
1 5
tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700
Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp
10 15 20
aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748
Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu
25 30 35 40
ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796
Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg
45 50 55
att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844
Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu
60 65 70
ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892
Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val
75 80 85
gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940
Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu
90 95 100
att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988

Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val	
105 110 115 120	
att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat	1036
Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn	
125 130 135	
ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc	1084
Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe	
140 145 150	
ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc	1132
Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro	
155 160 165	
ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct	1180
Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala	
170 175 180	
gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga	1228
Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg	
185 190 195 200	
gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga	1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly	
205 210 215	
att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga	1324
Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly	
220 225 230	
ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg	1372
Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg	
235 240 245	
aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc	1420
Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg	
250 255 260	
cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca	1468
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala	
265 270 275 280	
aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc	1516
Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe	
285 290 295	
ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg	1564
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly	
300 305 310	
ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat	1612
Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr	
315 320 325	
gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca	1660
Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr	

330	335	340	
ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc			1708
Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly			
345	350	355	360
atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc			1756
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr			
	365	370	375
tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat			1804
Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His			
	380	385	390
tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga			1852
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg			
	395	400	405
cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga			1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly			
	410	415	420
gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata			1948
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile			
	425	430	435
gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc			1996
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile			
	445	450	455
gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa			2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys			
	460	465	470
att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca			2092
Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr			
	475	480	485
gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa			2140
Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys			
	490	495	500
gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act			2188
Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr			
	505	510	515
gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg			2236
Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp			
	525	530	535
agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac			2284
Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His			
	540	545	550
tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca			2332
Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala			
	555	560	565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380
 Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe
 570 575 580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428
 Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu
 585 590 595 600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481
 Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
 605 610

gatattaata agcactcata ctaccaatta tcactaactt gccatttttt gtatgctgta 2541
 tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg tcttttctta 2601
 agtaattatg gtatatataa ggcggtggga aaaaacattt tataatgaaa gtatgtaggg 2661
 agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721
 tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa tgggtcaatga 2781
 tgaattacta atgccttatt ttctagggcat ataataatag tttagagaat gtagaccaga 2841
 taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901
 aacagtaggt ttcattccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961
 agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3007

<210> 81

<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu
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Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln
 20 25 30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys
 35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln
 50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser
 65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu
 85 90 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100

105

110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys
 115 120 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser
 130 135 140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile
 145 150 155 160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro
 165 170 175

Thr Glu Met Asp Glu Asn Glu Ser
 180

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285)..(836)

<400> 82

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gcgcgcgcgg gagcgcggga ggatcggcgg ctcgcggtca ctggtcacctg gctcgggttcc 120

ccgcaccccg gggctcacac ttaccgcgcg ggaggagcag cggccgggtg tccacccccca 180

tcctgcgccc agtctcctcg attcccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag ccccagggtg gccttggtgca catc atg acc agt ttt 296
 Met Thr Ser Phe
 1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344
 Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val
 5 10 15 20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392
 Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe
 25 30 35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440
 Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn
 40 45 50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488
 Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val
 55 60 65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln	Phe	Ser	Leu	Gln	Leu	Phe	Lys	Lys	Phe	Asn	Ser	Ser	Val	Leu	Ser		
70						75				80							
ttt	gaa	ata	aaa	aat	atg	agt	aaa	aag	acc	aat	ctg	atc	gtg	gac	agc	584	
Phe	Glu	Ile	Lys	Asn	Met	Ser	Lys	Lys	Thr	Asn	Leu	Ile	Val	Asp	Ser		
85					90					95					100		
aga	gag	ctg	ggc	tac	cta	aat	aaa	atg	gac	ctg	cca	tac	agg	tgc	atg	632	
Arg	Glu	Leu	Gly	Tyr	Leu	Asn	Lys	Met	Asp	Leu	Pro	Tyr	Arg	Cys	Met		
				105					110					115			
gtc	aga	ttc	gga	gag	tat	cag	ttt	ctg	atg	gag	aag	gaa	gat	ggc	gag	680	
Val	Arg	Phe	Gly	Glu	Tyr	Gln	Phe	Leu	Met	Glu	Lys	Glu	Asp	Gly	Glu		
			120					125						130			
tca	ttg	gaa	ttt	ttt	gag	act	caa	ttt	att	tta	tct	cca	aga	tca	ctc	728	
Ser	Leu	Glu	Phe	Phe	Glu	Thr	Gln	Phe	Ile	Leu	Ser	Pro	Arg	Ser	Leu		
			135				140					145					
ttg	caa	gaa	aac	aac	tgg	cca	cca	cac	agg	ccc	ata	ccg	gag	tat	ggc	776	
Leu	Gln	Glu	Asn	Asn	Trp	Pro	Pro	His	Arg	Pro	Ile	Pro	Glu	Tyr	Gly		
			150			155					160						
act	tat	tcg	ctc	tgc	tcc	tcc	caa	agc	agt	tct	ccg	aca	gaa	atg	gat	824	
Thr	Tyr	Ser	Leu	Cys	Ser	Ser	Gln	Ser	Ser	Ser	Pro	Thr	Glu	Met	Asp		
165					170				175					180			
gaa	aat	gag	tca	tgaacacaga	aagtctaaga	ggagaaatat	gatggatgaa									876	
Glu	Asn	Glu	Ser														
gagctctgta	gatgctgtat	agacactaaa	taagagttga	ttagggtagt	atattatagt	936											
catctgttat	gctgtgaaat	ttggaattca	gtattatcat	tttgaagtct	gtaaatgtg	996											
ttagtcatta	acttagtcac	ctgttgatt	ctggatctac	acaaaattat	tttaactgct	1056											
cttattaatc	tgtgaggatt	aatatacaaa	aagtatcctt	tgagatgaag	tcgtgttctc	1116											
aaaataaggt	tatattat	tctttttctg	cttgattttc	atcttggtt	ttgctttgtt	1176											
tttgtaagga	accatctctt	ggtttggtca	catcagttca	caacagccat	ttgttttcaa	1236											
ggccaaggct	ccaggcaggt	tgttactggt	gtttgcagcc	gttcagtact	tgcaagtactg	1296											
gaataggttc	taggctagt	tctgcgcgtc	actgtggtt	tagcatggga	ggacttattt	1356											
gagaaatact	accttacttt	tctatgattt	ctttttacag	agttatagt	tgtttactcc	1416											
taagatgaca	gttctctttg	tctatattca	gcatactaaga	caaataattta	aacatttttaa	1476											
agaaccactg	tgtaagttt	aggattat	acttacaaa	ttagaagttt	gacttttatg	1536											
tggtatacac	aatcttaaaa	tttcacgaat	tcacctttt	aatagtatcc	atgtacataa	1596											
taaaatcaaa	gtttaattag	c				1617											

<210> 83
 <211> 392
 <212> PRT
 <213> Homo sapiens

<400> 83
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 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
 275 280 285
 Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
 290 295 300
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
 305 310 315 320
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
 325 330 335
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
 340 345 350
 Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
 355 360 365
 Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
 370 375 380
 Val Glu Ser Pro Val Gln Lys Val
 385 390

<210> 84
 <211> 1898
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (119)..(1294)

<400> 84
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 gcgcggggccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118
 atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65	70	75	80	
gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc				406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro				
	85	90	95	
cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg				454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu				
	100	105	110	
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg				502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val				
	115	120	125	
ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca				550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser				
	130	135	140	
ccg ggt gag cgc ttt acg gac tgc cag ttc ctg gtg cta atg aac cga				598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg				
	145	150	155	160
gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag				646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln				
	165	170	175	
ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc				694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser				
	180	185	190	
aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc				742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser				
	195	200	205	
ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg				790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met				
	210	215	220	
ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac				838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr				
	225	230	235	240
ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc				886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser				
	245	250	255	
agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc				934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu				
	260	265	270	
ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc				982
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr				
	275	280	285	
cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc				1030
Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu				
	290	295	300	

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
 305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
 325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
 340 345 350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222
 Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
 355 360 365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270
 Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
 370 375 380

gtt gag tct cct gtg cag aag gtt tgaggggtgga aagggcctga ggggtgaagt 1324
 Val Glu Ser Pro Val Gln Lys Val
 385 390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgagggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agttttattct 1504

gagccccggg ggtagacagt cctcagttag gggttttggg gagtttgggg tcaagagagc 1564

ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctgctgtgc 1624

tctgccacct tccagactca ctcccctctg caaataacctg catttcttac cctggtgaga 1684

aaagcacaag cgggtgtagc tccaatgctg ctttcccagg aggggaaga tgggtgctgtg 1744

ctgaggaaag gggatgcaga gccctgccca gcaccaccac ctcctatgct cctggatccc 1804

taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta actttttgct 1864

cttataatth tttttatta aattaaatta ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270
 Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
 275 280 285
 Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
 290 295 300
 Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
 305 310 315 320
 Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
 325 330 335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
 340 345 350
 Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
 355 360 365
 Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
 370 375 380
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
 385 390 395 400
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
 405 410 415
 Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
 420 425 430

<210> 86
 <211> 2018
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (119)..(1414)

<400> 86
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 atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg	454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu	
100 105 110	
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg	502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val	
115 120 125	
ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca	550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser	
130 135 140	
ccg ggt gag cgc ttt acg gac tgc cag ttc ctg gtg cta atg aac cga	598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg	
145 150 155 160	
gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag	646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln	
165 170 175	
ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc	694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser	
180 185 190	
aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc	742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser	
195 200 205	
ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg	790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met	
210 215 220	
ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac	838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr	
225 230 235 240	
ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc	886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser	
245 250 255	
agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc	934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	
260 265 270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg	982
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	
275 280 285	
cag gat gcc ctg ttt gcc tat aag atg tca tgc gtg cag atg atg ttt	1030
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	
290 295 300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa	1078
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	
305 310 315 320	

cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag	1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	
325 330 335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag	1174
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln	
340 345 350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc	1222
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr	
355 360 365	
atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt	1270
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu	
370 375 380	
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg	1318
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val	
385 390 395 400	
gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag	1366
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys	
405 410 415	
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt	1414
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val	
420 425 430	
tgagggtgga aagggcctga ggggtgaagt gaaataggac cctccaccca tccccttctg	1474
ctgtaacctc tgaggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca	1534
gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgccttaag	1594
tcacccatct tccagtaagc agtttattct gagccccggg ggtagacagt cctcagttag	1654
gggttttggg gagtttggg tcaagagagc ataggtaggt tccacagtta ctcttcccac	1714
aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctcccctctg	1774
caaatacctg catttcttac cctggtgaga aaagcacaag cgggtgtaggc tccaatgctg	1834
ctttcccagg aggggtgaaga tgggtgctgtg ctgaggaaag gggatgcaga gccctgccc	1894
gcaccaccac ctctatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt	1954
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ctgc	2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser
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Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser
20 25 30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His
35 40 45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser
50 55 60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys
65 70 75 80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val
85 90 95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe
100 105 110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala
115 120 125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu
130 135 140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser
145 150 155 160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu
165 170 175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile
180 185 190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg
195 200 205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu
210 215 220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala
225 230 235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111)..(815)

<400> 88

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aaatgctgag aaatacataa agtttttctc ttctgccttg gatatttata atg ggt	116
Met Gly	
1	
atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt	164
Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly	
5 10 15	
aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc	212
Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser	
20 25 30	
aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat	260
Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn	
35 40 45 50	
aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa	308
Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu	
55 60 65	
gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg	356
Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val	
70 75 80	
ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat	404
Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn	
85 90 95	
ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag	452
Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu	
100 105 110	
atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat	500
Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn	
115 120 125 130	
ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat	548
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp	
135 140 145	
act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac	596
Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn	
150 155 160	
agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat	644
Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn	
165 170 175	
ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc	692
Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala	
180 185 190	
tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt	740
Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe	
195 200 205 210	

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga 788
 Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg
 215 220 225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat 835
 Asn Met Val Gln Arg Gln Phe Ile Ala
 230 235

gtggctggct cttgttttgt aaaccaaattg attaatcttc acttgagaaa gcagtttcta 895
 ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955
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 taagcattcg ggtactatca cccagaaata tgaattgcca gaatagaaca tttagcatgt 1315
 taagcgttga tgcataataa atcagaaata gatgtgagaa tgggtggaact ttttaaaaga 1375
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 aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgcccata 1855
 tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggtcatgtc 1915
 atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcca 1975
 ctgaggatga atgtaactgt gggcaaaacta tttaccctcc tttatctgtg aaatgaaagg 2035
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 cacaaaaggg aacaagcaaa aaagtttggg ttcgataaag tgatatgtaa tagttgcaga 2155
 aggctttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt 2215
 tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275
 tcttaaaaat aaatttttat agagatcctt gagtaaagac attttgctta atttcttttt 2335

tcttattccc cacttgtata tcccctacca gtaccgggat ctgcacacat ctttttgcag 2395
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 tcctattctg ttagtactta ttagaggagg agatggtttt cattgcatag tgacattttc 2515
 ttagccttaa cgttctgata gtagcttact actcacttct ctttttcagt tttcataata 2575
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 aaaataaatg tttttattct tt 2717

<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
 20 25 30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
 35 40 45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
 50 55 60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65 70 75 80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
 85 90 95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
 100 105 110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
 115 120 125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
 130 135 140

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
 145 150 155 160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
 165 170 175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
 180 185 190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
 195 200 205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
 210 215 220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
 225 230 235 240

Gln Tyr Glu Ile Val
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<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60)..(794)

<400> 90

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atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt 107
 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
 1 5 10 15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155
 Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
 20 25 30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203
 Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
 35 40 45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251
 Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
 50 55 60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299
 Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65 70 75 80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347
 Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
 85 90 95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395
 Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
 100 105 110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443
 Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
 115 120 125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta 491
Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
130 135 140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539
Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145 150 155 160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587
Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
165 170 175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635
Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
180 185 190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683
Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
195 200 205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg 731
Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
210 215 220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac 779
Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225 230 235 240

cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc totaccttta 834
Gln Tyr Glu Ile Val
245

aggacattta gggccccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894

tacttactga tagaccaaaa aactacacca gtagggtgat tcaatcaaga tgtatgtaga 954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014

atcaagatgt atgtttgcta tgttctaagt ccaccttcta tcccattcat gttagatcgt 1074

tgaaaccctg tatccctctg aaacactgga agagctagta aattgtaaat gaagtaatac 1134

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gctattttga tgtagtgta caagatggaa aattgattcc tctgactttg ctattgatgt 1254

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gattgtataa tttgcaccaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg 1374

cagagagtca catttgttaa tttaatttca gtcagtcaat agatggcatc cctcatcagg 1434

gttgccagat ggtgataaca gtgtaaggcc ttgggtctaa ggcatccacg actggaaggg 1494

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 tttagctggt accaggttga tatgacttgt caatattatg gtcaacttta agtcttagtt 1734
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 <212> PRT
 <213> Homo sapiens

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 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
 35 40 45
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 50 55 60
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 65 70 75 80
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 85 90 95
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 100 105 110
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 115 120 125
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 130 135 140
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 145 150 155 160
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 165 170 175
 Ala Leu Leu Gln
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<210> 92
 <211> 970
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (26)..(565)

<400> 92

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Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
 10                      15                      20                      25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
                      30                      35                      40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
                      45                      50                      55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
                      60                      65                      70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
                      75                      80                      85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
 90                      95                      100                      105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
                      110                      115                      120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
                      125                      130                      135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
                      140                      145                      150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
                      155                      160                      165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
170                      175                      180

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 tcccaccctg agattgggca tggggtgctg tgtggggggc atgtgctgcc tgttggtatg 885
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 <213> Homo sapiens

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 Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu
 35 40 45
 Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
 50 55 60
 Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
 65 70 75 80
 Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
 85 90 95
 Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
 100 105 110
 Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly
 115 120 125
 Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
 130 135 140
 Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala
 145 150 155 160
 Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
 165 170 175
 Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
 180 185 190
 Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
 195 200 205
 Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile

210	215	220
Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr		
225	230	235 240
Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala		
	245	250 255
Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr		
	260	265 270
Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu		
	275	280 285
Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu		
	290	295 300
Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln		
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Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His		
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 tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177
 Met
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 gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225
 Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg
 5 10 15
 gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273
 Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu
 20 25 30
 gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321
 Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala
 35 40 45
 gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369
 Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile
 50 55 60 65

gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt	417
Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe	
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Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu	
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aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc	513
Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys	
100 105 110	
acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc	561
Thr Ile Ser Asn Val Val Ser Ser Thr Gly Ala Ala Ser Gly Ile	
115 120 125	
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Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser	
130 135 140 145	
ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg	657
Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val	
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Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala	
165 170 175	
gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag	753
Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys	
180 185 190	
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Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu	
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ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt	849
Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg	
210 215 220 225	
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Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp	
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cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc	945
Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly	
245 250 255	
acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act	993
Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr	
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tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca	1041
Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser	
275 280 285	

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Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg
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cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137
Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile
310 315 320
tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc 1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His
325 330
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<213> Homo sapiens

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20 25 30
Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
35 40 45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
 50 55 60
 Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
 65 70 75 80
 Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
 85 90 95
 His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
 100 105 110
 Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
 115 120 125
 Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
 130 135 140
 Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
 145 150 155 160
 Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
 165 170 175
 Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
 180 185 190
 Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
 195 200 205
 Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
 210 215 220
 Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
 225 230 235 240
 Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
 245 250 255
 Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
 260 265 270
 Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
 275 280 285
 Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
 290 295 300
 Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
 305 310 315 320
 Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
 325 330 335
 Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
 340 345 350

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
 355 360 365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
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Val Cys Lys Tyr Lys Leu Leu
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<210> 96
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atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228
 Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
 1 5 10 15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276
 Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
 20 25 30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324
 Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
 35 40 45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372
 Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
 50 55 60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420
 Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
 65 70 75 80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468
 Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
 85 90 95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516
 His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
 100 105 110

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ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg 145 150 155 160	660
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ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys 195 200 205	804
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cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp 275 280 285	1044
ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly 290 295 300	1092
aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu 305 310 315 320	1140
atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu 325 330 335	1188

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236
 Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
 340 345 350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca 1284
 Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
 355 360 365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332
 Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
 370 375 380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380
 Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
 385 390 395 400

gtg tgc aaa tat aaa cta tta taaaatcg 1409
 Val Cys Lys Tyr Lys Leu Leu
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<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
 1 5 10 15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
 20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
 35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
 50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
 65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
 85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
 100 105 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
 115 120 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val
 130 135 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
 145 150 155 160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
 165 170 175
 Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
 180 185 190
 Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
 195 200 205
 Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
 210 215 220
 Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
 225 230 235 240
 Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
 245 250 255
 Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
 260 265 270
 Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
 275 280 285
 Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
 290 295 300
 Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
 305 310 315 320
 Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
 325 330 335
 Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
 340 345 350
 Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
 355 360 365
 Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
 370 375 380
 Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400
 Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415
 Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430
 His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
 435 440 445
 Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
 450 455 460

Asp
465

<210> 98
<211> 1940
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (477)..(1871)

<400> 98
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ccttggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180
tgggtgtatca ctggaggaaa tagcctgcc aaggaatacac gtcttcagaa gaagttctgt 240
gtggcttcaa gagactgata aaattgtgag aggaaaacag cctaccgggt cctcttttct 300
tcaatacaaa atgagataat aggggttggg aggaaaacct tcaagaccta tggaagtcag 360
ttgcagccag ctcatcacat agaggtgcag gtgaggtgta tttcatcac ggtggaaaat 420
tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg 479
Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
5 10 15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
20 25 30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
35 40 45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
50 55 60 65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
70 75 80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
85 90 95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu	Gln	Phe	His	Leu	Phe	Cys	Glu	Asp	Glu	Gly	Gln	Leu	Ile	Cys	Trp	
	100						105					110				
cgc	tgt	gag	cgg	gca	cca	cag	cac	aaa	ggg	cac	acc	aca	gct	ctt	gtt	863
Arg	Cys	Glu	Arg	Ala	Pro	Gln	His	Lys	Gly	His	Thr	Thr	Ala	Leu	Val	
	115					120					125					
gaa	gac	gta	tgc	cag	ggc	tac	aag	gaa	aag	ctc	cag	gaa	gct	gtg	aca	911
Glu	Asp	Val	Cys	Gln	Gly	Tyr	Lys	Glu	Lys	Leu	Gln	Glu	Ala	Val	Thr	
	130				135					140					145	
aaa	ctg	aag	caa	ctt	gaa	gac	aga	tgt	acg	gag	cag	aag	ctg	tcc	aca	959
Lys	Leu	Lys	Gln	Leu	Glu	Asp	Arg	Cys	Thr	Glu	Gln	Lys	Leu	Ser	Thr	
			150						155					160		
gca	atg	cga	ata	act	aaa	tgg	aaa	gag	aag	gta	cag	att	cag	aga	caa	1007
Ala	Met	Arg	Ile	Thr	Lys	Trp	Lys	Glu	Lys	Val	Gln	Ile	Gln	Arg	Gln	
			165					170					175			
aaa	atc	cgg	tct	gac	ttt	aag	aat	ctc	cag	tgt	ttc	cta	cat	gag	gaa	1055
Lys	Ile	Arg	Ser	Asp	Phe	Lys	Asn	Leu	Gln	Cys	Phe	Leu	His	Glu	Glu	
		180					185					190				
gag	aag	tct	tat	ctc	tgg	agg	ctg	gag	aaa	gaa	gaa	caa	cag	act	ctg	1103
Glu	Lys	Ser	Tyr	Leu	Trp	Arg	Leu	Glu	Lys	Glu	Glu	Gln	Gln	Thr	Leu	
	195					200					205					
agt	aga	ctg	agg	gac	tat	gag	gct	ggt	ctg	ggg	ctg	aag	agc	aat	gaa	1151
Ser	Arg	Leu	Arg	Asp	Tyr	Glu	Ala	Gly	Leu	Gly	Leu	Lys	Ser	Asn	Glu	
	210				215					220					225	
ctc	aag	agc	cac	atc	ctg	gaa	ctg	gag	gaa	aaa	tgt	cag	ggc	tca	gcc	1199
Leu	Lys	Ser	His	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Cys	Gln	Gly	Ser	Ala	
				230				235						240		
cag	aaa	ttg	ctg	cag	aat	gtg	aat	gac	act	ttg	agc	agg	agt	tgg	gct	1247
Gln	Lys	Leu	Leu	Gln	Asn	Val	Asn	Asp	Thr	Leu	Ser	Arg	Ser	Trp	Ala	
			245					250					255			
gtg	aag	ctg	gaa	aca	tca	gag	gct	gtc	tcc	ttg	gaa	ctt	cat	act	atg	1295
Val	Lys	Leu	Glu	Thr	Ser	Glu	Ala	Val	Ser	Leu	Glu	Leu	His	Thr	Met	
		260					265					270				
tgc	aat	gtt	tcc	aag	ctt	tac	ttc	gat	gtg	aag	aaa	atg	tta	agg	agt	1343
Cys	Asn	Val	Ser	Lys	Leu	Tyr	Phe	Asp	Val	Lys	Lys	Met	Leu	Arg	Ser	
	275					280					285					
cat	caa	gtt	agt	gtg	act	ctg	gat	cca	gat	aca	gct	cat	cac	gaa	cta	1391
His	Gln	Val	Ser	Val	Thr	Leu	Asp	Pro	Asp	Thr	Ala	His	His	Glu	Leu	
	290				295					300					305	
att	ctc	tct	gag	gat	cgg	aga	caa	gtg	act	cgt	gga	tac	acc	cag	gag	1439
Ile	Leu	Ser	Glu	Asp	Arg	Arg	Gln	Val	Thr	Arg	Gly	Tyr	Thr	Gln	Glu	
				310					315					320		
aat	cag	gac	aca	tct	tcc	agg	aga	ttt	act	gcc	ttc	ccc	tgt	gtc	ttg	1487
Asn	Gln	Asp	Thr	Ser	Ser	Arg	Arg	Phe	Thr	Ala	Phe	Pro	Cys	Val	Leu	

325

330

335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535
 Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
 340 345 350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583
 Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
 355 360 365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631
 Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
 370 375 380 385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679
 Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
 390 395 400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727
 Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
 405 410 415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775
 Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
 420 425 430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823
 Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
 435 440 445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
 Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
 450 455 460 465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag 1940

<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
 1 5 10 15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
 20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
 35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
 50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
 65 70 75 80
 Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
 85 90 95
 Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
 100 105 110
 Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
 115 120 125
 Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val
 130 135 140
 Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
 145 150 155 160
 Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
 165 170 175
 Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
 180 185 190
 Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
 195 200 205
 Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
 210 215 220
 Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
 225 230 235 240
 Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
 245 250 255
 Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
 260 265 270
 Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
 275 280 285
 Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
 290 295 300
 Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
 305 310 315 320
 Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
 325 330 335
 Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
 340 345 350
 Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
 355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
 370 375 380
 Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400
 Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415
 Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430
 His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
 435 440 445
 Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
 450 455 460
 Asp
 465

<210> 100
 <211> 1940
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (477)..(1871)

<400> 100
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 ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagagggggc 180
 tgggtgatca ctggaggaaa tagcctgcc aaggaatacac gtcttcagaa gaagttctgt 240
 gtggcttcaa gagactgatc aaattgtgag aggaaaacag cctacccggt cctcttttct 300
 tcaatacaaa atgagataat aggggttga aggaaaacct tcaagaccta tggaagtcag 360
 ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420
 tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479
 Met
 1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527
 Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
 5 10 15
 atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575
 Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
 20 25 30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa	623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln	
35 40 45	
aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca	671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro	
50 55 60 65	
ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att	719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile	
70 75 80	
gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga	767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly	
85 90 95	
gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg	815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp	
100 105 110	
cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt	863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val	
115 120 125	
gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca	911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr	
130 135 140 145	
aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca	959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr	
150 155 160	
gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa	1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln	
165 170 175	
aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa	1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu	
180 185 190	
gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg	1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu	
195 200 205	
agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa	1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu	
210 215 220 225	
ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc	1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala	
230 235 240	
cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct	1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala	
245 250 255	

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg	1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met	
260 265 270	
tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt	1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser	
275 280 285	
cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta	1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu	
290 295 300 305	
att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag	1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu	
310 315 320	
aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg	1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu	
325 330 335	
ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt	1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val	
340 345 350	
ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag	1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln	
355 360 365	
agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc	1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu	
370 375 380 385	
agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act	1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr	
390 395 400	
tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac	1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp	
405 410 415	
tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac	1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His	
420 425 430	
atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat	1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr	
435 440 445	
ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac	1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp	
450 455 460 465	
taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca	1931
taagggcag	1940

<210> 101
 <211> 685
 <212> PRT
 <213> Homo sapiens

<400> 101

Met	Glu	Leu	Leu	Arg	Thr	Ile	Thr	Tyr	Gln	Pro	Ala	Ala	Ser	Thr	Lys	1	5	10	15
Met	Cys	Glu	Gln	Ala	Leu	Gly	Lys	Gly	Cys	Gly	Ala	Asp	Ser	Lys	Lys	20	25	30	
Lys	Arg	Pro	Pro	Gln	Pro	Pro	Glu	Glu	Ser	Gln	Pro	Pro	Gln	Ser	Gln	35	40	45	
Ala	Gln	Val	Pro	Pro	Ala	Ala	Pro	His	His	His	His	His	His	Ser	His	50	55	60	
Ser	Gly	Pro	Glu	Ile	Ser	Arg	Ile	Ile	Val	Asp	Pro	Thr	Thr	Gly	Lys	65	70	75	80
Arg	Tyr	Cys	Arg	Gly	Lys	Val	Leu	Gly	Lys	Gly	Gly	Phe	Ala	Lys	Cys	85	90	95	
Tyr	Glu	Met	Thr	Asp	Leu	Thr	Asn	Asn	Lys	Val	Tyr	Ala	Ala	Lys	Ile	100	105	110	
Ile	Pro	His	Ser	Arg	Val	Ala	Lys	Pro	His	Gln	Arg	Glu	Lys	Ile	Asp	115	120	125	
Lys	Glu	Ile	Glu	Leu	His	Arg	Ile	Leu	His	His	Lys	His	Val	Val	Gln	130	135	140	
Phe	Tyr	His	Tyr	Phe	Glu	Asp	Lys	Glu	Asn	Ile	Tyr	Ile	Leu	Leu	Glu	145	150	155	160
Tyr	Cys	Ser	Arg	Arg	Ser	Met	Ala	His	Ile	Leu	Lys	Ala	Arg	Lys	Val	165	170	175	
Leu	Thr	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg	Gln	Ile	Val	Ser	Gly	180	185	190	
Leu	Lys	Tyr	Leu	His	Glu	Gln	Glu	Ile	Leu	His	Arg	Asp	Leu	Lys	Leu	195	200	205	
Gly	Asn	Phe	Phe	Ile	Asn	Glu	Ala	Met	Glu	Leu	Lys	Val	Gly	Asp	Phe	210	215	220	
Gly	Leu	Ala	Ala	Arg	Leu	Glu	Pro	Leu	Glu	His	Arg	Arg	Arg	Thr	Ile	225	230	235	240
Cys	Gly	Thr	Pro	Asn	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Asn	Lys	Gln	Gly	245	250	255	
His	Gly	Cys	Glu	Ser	Asp	Ile	Trp	Ala	Leu	Gly	Cys	Val	Met	Tyr	Thr	260	265	270	

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
 275 280 285
 Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
 290 295 300
 Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
 305 310 315 320
 Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
 325 330 335
 Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
 340 345 350
 Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
 355 360 365
 Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
 370 375 380
 His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
 385 390 395 400
 Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
 405 410 415
 Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
 420 425 430
 Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
 435 440 445
 Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
 450 455 460
 Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
 465 470 475 480
 Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
 485 490 495
 Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
 500 505 510
 Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
 515 520 525
 Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
 530 535 540
 His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
 545 550 555 560
 Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
 565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
 580 585 590
 Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
 595 600 605
 Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
 610 615 620
 Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
 625 630 635 640
 Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
 645 650 655
 Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
 660 665 670
 Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
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<220>
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 <222> (128)..(2182)

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 ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169
 Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser
 1 5 10
 acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217
 Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser
 15 20 25 30
 aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265
 Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln
 35 40 45
 tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313
 Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His
 50 55 60
 tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361
 Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr
 65 70 75
 ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca 409

Gly	Lys	Arg	Tyr	Cys	Arg	Gly	Lys	Val	Leu	Gly	Lys	Gly	Gly	Phe	Ala		
80						85					90						
aaa	tgt	tac	gag	atg	aca	gat	ttg	aca	aat	aac	aaa	gtc	tac	gcc	gca	457	
Lys	Cys	Tyr	Glu	Met	Thr	Asp	Leu	Thr	Asn	Asn	Lys	Val	Tyr	Ala	Ala		
95					100				105					110			
aaa	att	att	cct	cac	agc	aga	gta	gct	aaa	cct	cat	caa	agg	gaa	aag	505	
Lys	Ile	Ile	Pro	His	Ser	Arg	Val	Ala	Lys	Pro	His	Gln	Arg	Glu	Lys		
			115						120					125			
att	gac	aaa	gaa	ata	gag	ctt	cac	aga	att	ctt	cat	cat	aag	cat	gta	553	
Ile	Asp	Lys	Glu	Ile	Glu	Leu	His	Arg	Ile	Leu	His	His	Lys	His	Val		
			130					135					140				
gtg	cag	ttt	tac	cac	tac	ttc	gag	gac	aaa	gaa	aac	att	tac	att	ctc	601	
Val	Gln	Phe	Tyr	His	Tyr	Phe	Glu	Asp	Lys	Glu	Asn	Ile	Tyr	Ile	Leu		
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ttg	gaa	tac	tgc	agt	aga	agg	tca	atg	gct	cat	att	ttg	aaa	gca	aga	649	
Leu	Glu	Tyr	Cys	Ser	Arg	Arg	Ser	Met	Ala	His	Ile	Leu	Lys	Ala	Arg		
	160					165					170						
aag	gtg	ttg	aca	gag	cca	gaa	gtt	cga	tac	tac	ctc	agg	cag	att	gtg	697	
Lys	Val	Leu	Thr	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg	Gln	Ile	Val		
175					180					185					190		
tct	gga	ctg	aaa	tac	ctt	cat	gaa	caa	gaa	atc	ttg	cac	aga	gat	ctc	745	
Ser	Gly	Leu	Lys	Tyr	Leu	His	Glu	Gln	Glu	Ile	Leu	His	Arg	Asp	Leu		
			195						200					205			
aaa	cta	ggg	aac	ttt	ttt	att	aat	gaa	gcc	atg	gaa	cta	aaa	gtt	ggg	793	
Lys	Leu	Gly	Asn	Phe	Phe	Ile	Asn	Glu	Ala	Met	Glu	Leu	Lys	Val	Gly		
			210					215					220				
gac	ttc	ggt	ctg	gca	gcc	agg	cta	gaa	ccc	ttg	gaa	cac	aga	agg	aga	841	
Asp	Phe	Gly	Leu	Ala	Ala	Arg	Leu	Glu	Pro	Leu	Glu	His	Arg	Arg	Arg		
		225					230					235					
acg	ata	tgt	ggt	acc	cca	aat	tat	ctc	tct	cct	gaa	gtc	ctc	aac	aaa	889	
Thr	Ile	Cys	Gly	Thr	Pro	Asn	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Asn	Lys		
	240					245					250						
caa	gga	cat	ggc	tgt	gaa	tca	gac	att	tgg	gcc	ctg	ggc	tgt	gta	atg	937	
Gln	Gly	His	Gly	Cys	Glu	Ser	Asp	Ile	Trp	Ala	Leu	Gly	Cys	Val	Met		
255					260				265					270			
tat	aca	atg	tta	cta	ggg	agg	ccc	cca	ttt	gaa	act	aca	aat	ctc	aaa	985	
Tyr	Thr	Met	Leu	Leu	Gly	Arg	Pro	Pro	Phe	Glu	Thr	Thr	Asn	Leu	Lys		
			275						280					285			
gaa	act	tat	agg	tgc	ata	agg	gaa	gca	agg	tat	aca	atg	ccg	tcc	tca	1033	
Glu	Thr	Tyr	Arg	Cys	Ile	Arg	Glu	Ala	Arg	Tyr	Thr	Met	Pro	Ser	Ser		
			290					295					300				
ttg	ctg	gct	cct	gcc	aag	cac	tta	att	gct	agt	atg	ttg	tcc	aaa	aac	1081	
Leu	Leu	Ala	Pro	Ala	Lys	His	Leu	Ile	Ala	Ser	Met	Leu	Ser	Lys	Asn		

305	310	315	
cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe 320 325 330			1129
ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr 335 340 345 350			1177
gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys 355 360 365			1225
gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile 370 375 380			1273
gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu 385 390 395			1321
agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His 400 405 410			1369
agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser 415 420 425 430			1417
gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg 435 440 445			1465
atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys 450 455 460			1513
ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val 465 470 475			1561
ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys 480 485 490			1609
gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr 495 500 505 510			1657
tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly 515 520 525			1705
gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys 530 535 540			1753

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca	1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala	
545 550 555	
aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac	1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr	
560 565 570	
ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct	1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro	
575 580 585 590	
agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta	1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu	
595 600 605	
aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag	1993
Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln	
610 615 620	
gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat	2041
Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn	
625 630 635	
gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act	2089
Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr	
640 645 650	
ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa	2137
Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys	
655 660 665 670	
aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac	2182
Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn	
675 680 685	
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ggtttttcag acaattttgc agaaagggtgc attgattctt aaattctctc tgttgagagc	2482
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ctatggccat atataatattt ttttcattaa tttttgaaga tacttgtggc tggaaaagtg	2662
cattccttgt taataaactt tttatttatt acagcccaa gagcagtatt tattatcaaa	2722
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 <212> PRT
 <213> Homo sapiens

<400> 103
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 35 40 45
 Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
 50 55 60
 Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
 65 70 75 80
 Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
 85 90 95
 Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
 100 105 110
 Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
 115 120 125
 Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
 130 135 140
 Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
 145 150 155 160
 Leu

<210> 104
 <211> 1589
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (70)..(552)

<400> 104
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 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159
 Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
 Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
 35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
 Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
 50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
 Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
 65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351
 Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met
 80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
 Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
 115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
 130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
 Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
 145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
 Lys Arg Leu
 160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga gggtctgccc tgggtggtctc 652
 acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712
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 ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952
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 aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
 tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaattgat 1552
 tgggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

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 <211> 161
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
 35 40 45
 Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
 50 55 60
 Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
 65 70 75 80
 Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
 85 90 95
 Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
 100 105 110
 Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
 115 120 125
 Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
 130 135 140
 Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
 145 150 155 160
 Leu

<210> 106
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (70)..(552)

<400> 106
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 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
 1 5 10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159
 Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
 Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
 35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
 Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
 50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
 Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
 65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351
 Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met
 80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
 Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
 115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
 130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
 Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
 145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
 Lys Arg Leu

aagtcctttc cacctctcat ccagcttcac gcttggtgga ggttctgccc tgggtggtctc 652
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cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccttgagtcc tgccatctaa 832
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aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaagtat 1552
tggtgtcatt ttcccatttg ccaatgtagt ctcaatt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

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Leu	Asp	Pro	Pro	Thr	Asp	Leu	Lys	Phe	Lys	Gly	Pro	Phe	Thr	Asp	Val
			20					25					30		
Val	Thr	Thr	Asn	Leu	Lys	Leu	Arg	Asn	Pro	Ser	Asp	Arg	Lys	Val	Cys
			35				40					45			
Phe	Lys	Val	Lys	Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn
	50					55					60				
Ser	Gly	Ile	Ile	Asp	Pro	Gly	Ser	Thr	Val	Thr	Val	Ser	Val	Met	Leu
65					70					75				80	

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met
85 90 95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val
100 105 110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys
115 120 125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro
130 135 140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro
145 150 155 160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met
165 170 175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu
180 185 190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His
195 200 205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val
210 215 220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile
225 230 235 240

Gly Phe Phe Leu Gly Lys Phe Ile Leu
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<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(978)

<400> 108

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gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgcgctcgtc ccccgcccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237
Met Ala
1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285
Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333
 Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr
 20 25 30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381
 Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys
 35 40 45 50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429
 Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly
 55 60 65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477
 Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro
 70 75 80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525
 Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln
 85 90 95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573
 Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys
 100 105 110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621
 Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe
 115 120 125 130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669
 Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys
 135 140 145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717
 Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro
 150 155 160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765
 His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu
 165 170 175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813
 Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg
 180 185 190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861
 His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp
 195 200 205 210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909
 Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser
 215 220 225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957
 Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe
 230 235 240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt 1008
Phe Leu Gly Lys Phe Ile Leu
245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068
gcccacgggtg accattttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128
cttacgggta gaaaacacaa taaaaacaaa ctgttcgggt actggacagg ttgtatatta 1188
ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248
agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308
tgttattttta ataatccctt taaattttat ctgttgctgt tacctottga aatatgattt 1368
atntagattg ctaatcccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428
tgctctttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488
cttatccctt gtgaggcagt tgttgactga gtttttcac cttacaatcc tgtcccatgg 1548
tatttaacat aaaaaaaaaat aaaactgtta acagattcct gctcgat 1595

<210> 109
<211> 540
<212> PRT
<213> Homo sapiens

<400> 109
Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
20 25 30
Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
35 40 45
Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
50 55 60
His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
65 70 75 80
Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
85 90 95
Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
100 105 110
Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115 120 125
Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130		135		140
Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp				
145		150		160
Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn				
	165		170	175
Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro				
	180		185	190
Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu				
	195		200	205
Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg				
	210		215	220
Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala				
225		230		240
Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His				
	245		250	255
Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu				
	260		265	270
Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln				
	275		280	285
Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro				
	290		295	300
Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser				
305		310		315
Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu				
	325		330	335
Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly				
	340		345	350
Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys				
	355		360	365
Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys				
	370		375	380
Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala				
385		390		400
Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg				
	405		410	415
Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu				
	420		425	430
Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg				

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
 450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
 465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
 485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
 500 505 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
 515 520 525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
 530 535 540

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 110

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gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116
 Met Gly Thr Thr Ala
 1 5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164
 Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
 10 15 20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212
 Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
 25 30 35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
 Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
 40 45 50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
 Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
 55 60 65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
 Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
 70 75 80 85

ctc	caa	cag	gaa	aag	ctg	cta	cct	gcc	caa	ctc	cct	gct	gaa	aag	gaa	404
Leu	Gln	Gln	Glu	Lys	Leu	Leu	Pro	Ala	Gln	Leu	Pro	Ala	Glu	Lys	Glu	
				90					95					100		
gtg	ggt	ccc	cct	ctc	cct	cag	gaa	gct	gtc	ccc	ctc	caa	aaa	gag	ctg	452
Val	Gly	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Val	Pro	Leu	Gln	Lys	Glu	Leu	
			105					110					115			
ccc	tct	ctc	cag	cac	ccc	aat	gaa	cag	aag	gaa	gga	acg	cca	gct	cca	500
Pro	Ser	Leu	Gln	His	Pro	Asn	Glu	Gln	Lys	Glu	Gly	Thr	Pro	Ala	Pro	
		120					125					130				
ttt	ggg	gac	cag	agc	cat	cca	gaa	cct	gag	tcc	tgg	aat	gca	gcc	cag	548
Phe	Gly	Asp	Gln	Ser	His	Pro	Glu	Pro	Glu	Ser	Trp	Asn	Ala	Ala	Gln	
	135					140					145					
cac	tgc	caa	cag	gac	cgg	tcc	caa	ggg	ggc	tgg	ggc	cac	cgg	ctg	gat	596
His	Cys	Gln	Gln	Asp	Arg	Ser	Gln	Gly	Gly	Trp	Gly	His	Arg	Leu	Asp	
150				155					160					165		
ggc	ttc	ccc	cct	ggg	cgg	cct	tct	cca	gac	aat	ctg	aac	caa	atc	tgc	644
Gly	Phe	Pro	Pro	Gly	Arg	Pro	Ser	Pro	Asp	Asn	Leu	Asn	Gln	Ile	Cys	
			170						175					180		
ctt	cct	aac	cgt	cag	cat	gtg	gta	tat	ggt	ccc	tgg	aac	cta	cca	cag	692
Leu	Pro	Asn	Arg	Gln	His	Val	Val	Tyr	Gly	Pro	Trp	Asn	Leu	Pro	Gln	
			185					190					195			
tcc	agc	tac	tcc	cac	ctc	act	cgc	cag	ggt	gag	acc	ctc	aat	ttc	ctg	740
Ser	Ser	Tyr	Ser	His	Leu	Thr	Arg	Gln	Gly	Glu	Thr	Leu	Asn	Phe	Leu	
		200					205					210				
gag	att	gga	tat	tcc	cgc	tgc	tgc	cac	tgc	cgc	agc	cac	aca	aac	cgc	788
Glu	Ile	Gly	Tyr	Ser	Arg	Cys	Cys	His	Cys	Arg	Ser	His	Thr	Asn	Arg	
	215					220					225					
cta	gag	tgt	gcc	aaa	ctt	gtg	tgg	gag	gaa	gca	atg	agc	cga	ttc	tgt	836
Leu	Glu	Cys	Ala	Lys	Leu	Val	Trp	Glu	Glu	Ala	Met	Ser	Arg	Phe	Cys	
230					235					240					245	
gag	gcc	gag	ttc	tcg	gtc	aag	acc	cga	ccc	cac	tgg	tgc	tgc	acg	cgg	884
Glu	Ala	Glu	Phe	Ser	Val	Lys	Thr	Arg	Pro	His	Trp	Cys	Cys	Thr	Arg	
			250					255						260		
cag	ggg	gag	gct	cgg	ttc	tcc	tgc	ttc	cag	gag	gaa	gct	ccc	cag	cca	932
Gln	Gly	Glu	Ala	Arg	Phe	Ser	Cys	Phe	Gln	Glu	Glu	Ala	Pro	Gln	Pro	
		265						270					275			
cac	tac	cag	ctc	cgg	gcc	tgc	ccc	agc	cat	cag	cct	gat	att	tcc	tcg	980
His	Tyr	Gln	Leu	Arg	Ala	Cys	Pro	Ser	His	Gln	Pro	Asp	Ile	Ser	Ser	
		280				285						290				
ggt	ctt	gag	ctg	cct	ttc	cct	cct	ggg	gtg	ccc	aca	ttg	gac	aat	atc	1028
Gly	Leu	Glu	Leu	Pro	Phe	Pro	Pro	Gly	Val	Pro	Thr	Leu	Asp	Asn	Ile	
	295					300					305					
aag	aac	atc	tgc	cac	ctg	agg	cgc	ttc	cgc	tct	gtg	cca	cgc	aac	ctg	1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu	
310 315 320 325	
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg	1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu	
330 335 340	
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt	1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys	
345 350 355	
aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag	1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu	
360 365 370	
tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc	1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser	
375 380 385	
cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat	1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr	
390 395 400 405	
gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc	1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu	
410 415 420	
atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat	1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His	
425 430 435	
att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca	1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro	
440 445 450	
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc	1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile	
455 460 465	
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc	1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu	
470 475 480 485	
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc	1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile	
490 495 500	
aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc	1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala	
505 510 515	
aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc	1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser	
520 525 530	
acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga	1751
Thr Ser Glu Pro Lys Glu Glu	

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 111
 Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
 1 5 10 15
 Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
 20 25 30
 Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
 35 40 45
 Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
 50 55 60
 His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65 70 75 80
 Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
 85 90 95
 Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
 100 105 110
 Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
 115 120 125
 Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
 130 135 140
 Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
 145 150 155 160
 Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
 165 170 175
 Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
 180 185 190
 Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
 195 200 205
 Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
 210 215 220
 Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
 225 230 235 240
 Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His

245

250

255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
435 440 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
500 505 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
515 520 525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
530 535 540

<210> 112
 <211> 1810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (102)..(1721)

<400> 112

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gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116
 Met Gly Thr Thr Ala
 1 5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164
 Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
 10 15 20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212
 Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
 25 30 35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
 Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
 40 45 50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
 Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
 55 60 65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
 Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
 70 75 80 85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
 Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
 90 95 100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452
 Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
 105 110 115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500
 Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
 120 125 130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548
 Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
 135 140 145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596
 His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
 150 155 160 165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly	Phe	Pro	Pro	Gly	Arg	Pro	Ser	Pro	Asp	Asn	Leu	Asn	Gln	Ile	Cys	
				170					175					180		
ctt	cct	aac	cgt	cag	cat	gtg	gta	tat	ggg	ccc	tgg	aac	cta	cca	cag	692
Leu	Pro	Asn	Arg	Gln	His	Val	Val	Tyr	Gly	Pro	Trp	Asn	Leu	Pro	Gln	
			185					190					195			
tcc	agc	tac	tcc	cac	ctc	act	cgc	cag	ggg	gag	acc	ctc	aat	ttc	ctg	740
Ser	Ser	Tyr	Ser	His	Leu	Thr	Arg	Gln	Gly	Glu	Thr	Leu	Asn	Phe	Leu	
		200					205					210				
gag	att	gga	tat	tcc	cgc	tgc	tgc	cac	tgc	cgc	agc	cac	aca	aac	cgc	788
Glu	Ile	Gly	Tyr	Ser	Arg	Cys	Cys	His	Cys	Arg	Ser	His	Thr	Asn	Arg	
	215					220					225					
cta	gag	tgt	gcc	aaa	ctt	gtg	tgg	gag	gaa	gca	atg	agc	cga	ttc	tgt	836
Leu	Glu	Cys	Ala	Lys	Leu	Val	Trp	Glu	Glu	Ala	Met	Ser	Arg	Phe	Cys	
	230				235					240					245	
gag	gcc	gag	ttc	tgc	gtc	aag	acc	cga	ccc	cac	tgg	tgc	tgc	acg	cgg	884
Glu	Ala	Glu	Phe	Ser	Val	Lys	Thr	Arg	Pro	His	Trp	Cys	Cys	Thr	Arg	
				250					255					260		
cag	ggg	gag	gct	cgg	ttc	tcc	tgc	ttc	cag	gag	gaa	gct	ccc	cag	cca	932
Gln	Gly	Glu	Ala	Arg	Phe	Ser	Cys	Phe	Gln	Glu	Glu	Ala	Pro	Gln	Pro	
			265					270					275			
cac	tac	cag	ctc	cgg	gcc	tgc	ccc	agc	cat	cag	cct	gat	att	tcc	tgc	980
His	Tyr	Gln	Leu	Arg	Ala	Cys	Pro	Ser	His	Gln	Pro	Asp	Ile	Ser	Ser	
			280				285					290				
ggg	ctt	gag	ctg	cct	ttc	cct	cct	ggg	gtg	ccc	aca	ttg	gac	aat	atc	1028
Gly	Leu	Glu	Leu	Pro	Phe	Pro	Pro	Gly	Val	Pro	Thr	Leu	Asp	Asn	Ile	
	295					300					305					
aag	aac	atc	tgc	cac	ctg	agg	cgc	ttc	cgc	tct	gtg	cca	cgc	aac	ctg	1076
Lys	Asn	Ile	Cys	His	Leu	Arg	Arg	Phe	Arg	Ser	Val	Pro	Arg	Asn	Leu	
	310				315					320				325		
cca	gct	act	gac	ccc	cta	caa	agg	gag	ctg	ctg	gca	ctg	atc	cag	ctg	1124
Pro	Ala	Thr	Asp	Pro	Leu	Gln	Arg	Glu	Leu	Leu	Ala	Leu	Ile	Gln	Leu	
				330					335					340		
gag	agg	gag	ttc	cag	cgc	tgc	tgc	cgc	cag	ggg	aac	aat	cac	acc	tgt	1172
Glu	Arg	Glu	Phe	Gln	Arg	Cys	Cys	Arg	Gln	Gly	Asn	Asn	His	Thr	Cys	
			345					350					355			
aca	tgg	aag	gcc	tgg	gag	gat	acc	ctt	gac	aaa	tac	tgt	gac	cgg	gag	1220
Thr	Trp	Lys	Ala	Trp	Glu	Asp	Thr	Leu	Asp	Lys	Tyr	Cys	Asp	Arg	Glu	
			360				365					370				
tat	gct	gtg	aag	acc	cac	cac	cac	ttg	tgt	tgc	cgc	cac	cct	ccc	agc	1268
Tyr	Ala	Val	Lys	Thr	His	His	His	Leu	Cys	Cys	Arg	His	Pro	Pro	Ser	
	375					380					385					
cct	act	cgg	gat	gag	tgc	ttt	gcc	cgt	cgg	gct	cct	tac	ccc	aac	tat	1316
Pro	Thr	Arg	Asp	Glu	Cys	Phe	Ala	Arg	Arg	Ala	Pro	Tyr	Pro	Asn	Tyr	

390

395

400

405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364
 Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu
 410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412
 Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His
 425 430 435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460
 Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro
 440 445 450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508
 Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile
 455 460 465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556
 Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu
 470 475 480 485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604
 Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
 490 495 500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652
 Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
 505 510 515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700
 Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
 520 525 530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751
 Thr Ser Glu Pro Lys Glu Glu
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<210> 113

<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
 20 25 30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
 35 40 45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50

55

60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
290 295 300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser

355

360

365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
 370 375 380

<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 114

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attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
 1 5 10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
 15 20 25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
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gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
 45 50 55

ggg tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
 60 65 70 75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
 80 85 90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
 95 100 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
 110 115 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
 125 130 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac	665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr	
140 145 150 155	
atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg	713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu	
160 165 170	
atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc	761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys	
175 180 185	
aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc	809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro	
190 195 200	
acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg	857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val	
205 210 215	
tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc	905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly	
220 225 230 235	
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt	953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser	
240 245 250	
ggg gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat	1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr	
255 260 265	
ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct	1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro	
270 275 280	
cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc	1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg	
285 290 295	
aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca	1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala	
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gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat	1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His	
320 325 330	
gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta	1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu	
335 340 345	
gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct	1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro	
350 355 360	

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
 Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
 365 370 375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386
 Leu Glu Ile
 380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cggtaggaggt 1446
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<211> 382
<212> PRT
<213> Homo sapiens

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Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
35 40 45
Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
50 55 60
Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65 70 75 80
Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95
Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110
Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125
Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140
Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160
Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175
Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190
Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205
Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
290 295 300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
370 375 380

<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 116

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attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
1 5 10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
15 20 25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val	Leu	Phe	Ile	Phe	Arg	Ile	Leu	Leu	Leu	Gly	Thr	Ala	Val	Glu	Ser		
		30					35					40					
gcc	tgg	gga	gat	gag	cag	tct	gcc	ttt	cgt	tgt	aac	act	cag	caa	cct	377	
Ala	Trp	Gly	Asp	Glu	Gln	Ser	Ala	Phe	Arg	Cys	Asn	Thr	Gln	Gln	Pro		
	45					50				55							
ggc	tgt	gaa	aat	gtc	tgc	tat	gac	aag	tct	ttc	cca	atc	tct	cat	gtg	425	
Gly	Cys	Glu	Asn	Val	Cys	Tyr	Asp	Lys	Ser	Phe	Pro	Ile	Ser	His	Val		
	60				65				70						75		
cgc	ttc	tgg	gtc	ctg	cag	atc	ata	ttt	gtg	tct	gta	ccc	aca	ctc	ttg	473	
Arg	Phe	Trp	Val	Leu	Gln	Ile	Ile	Phe	Val	Ser	Val	Pro	Thr	Leu	Leu		
			80						85						90		
tac	ctg	gct	cat	gtg	ttc	tat	gtg	atg	cga	aag	gaa	gag	aaa	ctg	aac	521	
Tyr	Leu	Ala	His	Val	Phe	Tyr	Val	Met	Arg	Lys	Glu	Glu	Lys	Leu	Asn		
			95					100					105				
aag	aaa	gag	gaa	gaa	ctc	aag	gtt	gcc	caa	act	gat	ggc	gtc	aat	gtg	569	
Lys	Lys	Glu	Glu	Glu	Leu	Lys	Val	Ala	Gln	Thr	Asp	Gly	Val	Asn	Val		
		110					115					120					
gac	atg	cac	ttg	aag	cag	att	gag	ata	aag	aag	ttc	aag	tac	ggc	att	617	
Asp	Met	His	Leu	Lys	Gln	Ile	Glu	Ile	Lys	Lys	Phe	Lys	Tyr	Gly	Ile		
	125					130					135						
gaa	gag	cat	ggc	aag	gtg	aaa	atg	cga	ggg	ggg	ttg	ctg	cga	acc	tac	665	
Glu	Glu	His	Gly	Lys	Val	Lys	Met	Arg	Gly	Gly	Leu	Leu	Arg	Thr	Tyr		
	140				145					150					155		
atc	atc	agt	atc	ctc	ttc	aag	tct	atc	ttt	gag	gtg	gcc	ttc	ttg	ctg	713	
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atc	cag	tgg	tac	atc	tat	gga	ttc	agc	ttg	agt	gct	gtt	tac	act	tgc	761	
Ile	Gln	Trp	Tyr	Ile	Tyr	Gly	Phe	Ser	Leu	Ser	Ala	Val	Tyr	Thr	Cys		
			175					180					185				
aaa	aga	gat	ccc	tgc	cca	cat	cag	gtg	gac	tgt	ttc	ctc	tct	cgc	ccc	809	
Lys	Arg	Asp	Pro	Cys	Pro	His	Gln	Val	Asp	Cys	Phe	Leu	Ser	Arg	Pro		
		190					195					200					
acg	gag	aaa	acc	atc	ttc	atc	atc	ttc	atg	ctg	gtg	gtg	tcc	ttg	gtg	857	
Thr	Glu	Lys	Thr	Ile	Phe	Ile	Ile	Phe	Met	Leu	Val	Val	Ser	Leu	Val		
	205					210					215						
tcc	ctg	gcc	ttg	aat	atc	att	gaa	ctc	ttc	tat	gtt	ttc	ttc	aag	ggc	905	
Ser	Leu	Ala	Leu	Asn	Ile	Ile	Glu	Leu	Phe	Tyr	Val	Phe	Phe	Lys	Gly		
	220				225					230					235		
gtt	aag	gat	cgg	gtt	aag	gga	aag	agc	gac	cct	tac	cat	gcg	acc	agt	953	
Val	Lys	Asp	Arg	Val	Lys	Gly	Lys	Ser	Asp	Pro	Tyr	His	Ala	Thr	Ser		
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ggc	gcg	ctg	agc	cct	gcc	aaa	gac	tgt	ggg	tct	caa	aaa	tat	gct	tat	1001	
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255

260

265

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 Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
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cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
 Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
 285 290 295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145
 Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala
 300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
 Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
 320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
 Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
 335 340 345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
 Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
 350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
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 365 370 375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386
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 380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cgggtggaggt 1446

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gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

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tcagttttaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

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 ctaatttgtt tgacattcca tgtaaaacta cggtcatggt cagcttcatt gcatgtaatg 3006
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 tttagtat 3074

<210> 117
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 117
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 Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala
 20 25 30
 Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
 35 40 45
 Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
 50 55 60
 Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
 65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
 85 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
 100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
 115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
 130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
 145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
 165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
 180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
 195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
 210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
 225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
 245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
 260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
 275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
 290 295 300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
 305 310 315 320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
 325 330 335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
 340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
 355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
 370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
 385 395 395

<210> 118
 <211> 2054
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)..(1269)

<400> 118
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aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111
 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
 1 5 10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159
 Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu
 15 20 25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207
 Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
 30 35 40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255
 Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45 50 55 60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303
 Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
 65 70 75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351
 Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
 80 85 90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
 Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
 95 100 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
 110 115 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
 125 130 135 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
 Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
 145 150 155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg	Leu	Arg	Ala	Leu	Ala	Asp	Gly	Val	Gln	Lys	Val	His	Lys	Gly	Thr		
			160					165						170			
acc	atc	gcc	aat	gtg	gtg	tct	ggc	tct	ctc	agc	att	tcc	tct	ggc	atc	639	
Thr	Ile	Ala	Asn	Val	Val	Ser	Gly	Ser	Leu	Ser	Ile	Ser	Ser	Gly	Ile		
		175					180					185					
ctg	acc	ctc	gtc	ggc	atg	ggt	ctg	gca	ccc	ttc	aca	gag	gga	ggc	agc	687	
Leu	Thr	Leu	Val	Gly	Met	Gly	Leu	Ala	Pro	Phe	Thr	Glu	Gly	Gly	Ser		
	190					195					200						
ctt	gta	ctc	ttg	gaa	cct	ggg	atg	gag	ttg	gga	atc	aca	gca	gct	ttg	735	
Leu	Val	Leu	Leu	Glu	Pro	Gly	Met	Glu	Leu	Gly	Ile	Thr	Ala	Ala	Leu		
205					210					215					220		
acc	ggg	att	acc	agc	agt	acc	ata	gac	tac	gga	aag	aag	tgg	tgg	aca	783	
Thr	Gly	Ile	Thr	Ser	Ser	Thr	Ile	Asp	Tyr	Gly	Lys	Lys	Trp	Trp	Thr		
			225					230						235			
caa	gcc	caa	gcc	cac	gac	ctg	gtc	atc	aaa	agc	ctt	gac	aaa	ttg	aag	831	
Gln	Ala	Gln	Ala	His	Asp	Leu	Val	Ile	Lys	Ser	Leu	Asp	Lys	Leu	Lys		
		240						245					250				
gag	gtg	aag	gag	ttt	ttg	ggt	gag	aac	ata	tcc	aac	ttt	ctt	tcc	tta	879	
Glu	Val	Lys	Glu	Phe	Leu	Gly	Glu	Asn	Ile	Ser	Asn	Phe	Leu	Ser	Leu		
	255						260					265					
gct	ggc	aat	act	tac	caa	ctc	aca	cga	ggc	att	ggg	aag	gac	atc	cgt	927	
Ala	Gly	Asn	Thr	Tyr	Gln	Leu	Thr	Arg	Gly	Ile	Gly	Lys	Asp	Ile	Arg		
	270				275						280						
gcc	ctc	aga	cga	gcc	aga	gcc	aat	ctt	cag	tca	gta	ccg	cat	gcc	tca	975	
Ala	Leu	Arg	Arg	Ala	Arg	Ala	Asn	Leu	Gln	Ser	Val	Pro	His	Ala	Ser		
285					290					295					300		
gcc	tca	cgc	ccc	cgg	gtc	act	gag	cca	atc	tca	gct	gaa	agc	ggt	gaa	1023	
Ala	Ser	Arg	Pro	Arg	Val	Thr	Glu	Pro	Ile	Ser	Ala	Glu	Ser	Gly	Glu		
			305						310					315			
cag	gtg	gag	aga	gtt	aat	gaa	ccc	agc	atc	ctg	gaa	atg	agc	aga	gga	1071	
Gln	Val	Glu	Arg	Val	Asn	Glu	Pro	Ser	Ile	Leu	Glu	Met	Ser	Arg	Gly		
		320						325					330				
gtc	aag	ctc	acg	gat	gtg	gcc	cct	gta	agc	ttc	ttt	ctt	gtg	ctg	gat	1119	
Val	Lys	Leu	Thr	Asp	Val	Ala	Pro	Val	Ser	Phe	Phe	Leu	Val	Leu	Asp		
	335						340					345					
gta	gtc	tac	ctc	gtg	tac	gaa	tca	aag	cac	tta	cat	gag	ggg	gca	aag	1167	
Val	Val	Tyr	Leu	Val	Tyr	Glu	Ser	Lys	His	Leu	His	Glu	Gly	Ala	Lys		
	350					355					360						
tca	gag	aca	gct	gag	gag	ctg	aag	aag	gtg	gct	cag	gag	ctg	gag	gag	1215	
Ser	Glu	Thr	Ala	Glu	Glu	Leu	Lys	Lys	Val	Ala	Gln	Glu	Leu	Glu	Glu		
365					370				375						380		
aag	cta	aac	att	ctc	aac	aat	aat	tat	aag	att	ctg	cag	gcg	gac	caa	1263	
Lys	Leu	Asn	Ile	Leu	Asn	Asn	Asn	Tyr	Lys	Ile	Leu	Gln	Ala	Asp	Gln		

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319
 Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggtccac tacagacca gcccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatgg cccctgcctt gtctttccag catccactct 1679

cccttgcctt cctgggggca tatctcagtc aggcagcggc ttcttgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct cttagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcac 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

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Ser	Ala	Leu	Phe	Leu	Gly	Val	Arg	Val	Arg	Ala	Glu	Glu	Ala	Gly	Ala
			20					25					30		
Arg	Val	Gln	Gln	Asn	Val	Pro	Ser	Gly	Thr	Asp	Thr	Gly	Asp	Pro	Gln
		35					40					45			
Ser	Lys	Pro	Leu	Gly	Asp	Trp	Ala	Ala	Gly	Thr	Met	Asp	Pro	Glu	Ser
	50				55						60				
Ser	Ile	Phe	Ile	Glu	Asp	Ala	Ile	Lys	Tyr	Phe	Lys	Glu	Lys	Val	Ser
	65				70					75					80
Thr	Gln	Asn	Leu	Leu	Leu	Leu	Leu	Thr	Asp	Asn	Glu	Ala	Trp	Asn	Gly
			85					90						95	
Phe	Val	Ala	Ala	Ala	Glu	Leu	Pro	Arg	Asn	Glu	Ala	Asp	Glu	Leu	Arg

100

105

110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
 115 120 125
 Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
 130 135 140
 Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
 145 150 155 160
 Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
 165 170 175
 Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
 180 185 190
 Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
 195 200 205
 Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
 210 215 220
 Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
 225 230 235 240
 His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
 245 250 255
 Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
 260 265 270
 Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
 275 280 285
 Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
 290 295 300
 Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
 305 310 315 320
 Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
 325 330 335
 Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
 340 345 350
 Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
 355 360 365
 Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
 370 375 380
 Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
 385 390 395

<210> 120
 <211> 2054
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)..(1269)

<400> 120
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 aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111
 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
 1 5 10
 tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159
 Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu
 15 20 25
 gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207
 Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
 30 35 40
 gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255
 Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45 50 55 60
 gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303
 Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
 65 70 75
 gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351
 Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
 80 85 90
 gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
 Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
 95 100 105
 gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
 110 115 120
 aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
 125 130 135 140
 ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
 Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
 145 150 155
 agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
 Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
 160 165 170
 acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile	
175	180 185
ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc	687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser	
190	195 200
ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg	735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu	
205	210 215 220
acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca	783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr	
	225 230 235
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag	831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys	
	240 245 250
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta	879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu	
	255 260 265
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt	927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg	
	270 275 280
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca	975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser	
	285 290 295 300
gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa	1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu	
	305 310 315
cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga	1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly	
	320 325 330
gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat	1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp	
	335 340 345
gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag	1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys	
	350 355 360
tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag	1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu	
	365 370 375 380
aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa	1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln	
	385 390 395
gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca	1319
Glu Leu	

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379
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 aaaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499
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 aactgaagg gcagggtgtg agccatggcc atgggtccca gctgaggagc aggtgtcctt 1859
 gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919
 cttacccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979
 gctcagatct cttagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039
 actcacctac tcac 2054

<210> 121
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 121
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 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
 20 25 30
 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35 40 45
 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50 55 60
 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65 70 75 80
 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85 90 95
 Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
 100 105

<210> 122

<211> 1546
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (89)..(412)

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 Met Gly Val Gln Val Glu Thr Ile
 1 5
 tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160
 Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val
 10 15 20
 gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208
 Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser
 25 30 35 40
 cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256
 Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val
 45 50 55
 atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304
 Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg
 60 65 70
 gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352
 Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His
 75 80 85
 cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400
 Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
 90 95 100
 cta aaa ctg gaa tgacaggaat ggccctctcc cttagctccc tgttcttgga 452
 Leu Lys Leu Glu
 105
 tctgccatgg agggatctgg tgccctccaga catgtgcaca tgaatccata tggagctttt 512
 cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572
 agctttgctt ccgacacctc tgtttctctt tcccctttct cctcgatatgt gtgtttacct 632
 aaactatatg ccataaacct caagttactc attttatttt gttttcattt tgggggtgaag 692
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 tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc agggacctct 1112
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<210> 123
 <211> 679
 <212> PRT
 <213> Homo sapiens

<400> 123
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 Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala
 20 25 30
 Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe
 35 40 45
 Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile
 50 55 60
 Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys
 65 70 75 80
 Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn
 85 90 95
 Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly
 100 105 110
 Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
 115 120 125
 Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
 130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met
 145 150 155 160
 Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
 165 170 175
 Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
 180 185 190
 Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
 195 200 205
 Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
 210 215 220
 Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
 225 230 235 240
 Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
 245 250 255
 Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
 260 265 270
 Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
 275 280 285
 Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
 290 295 300
 Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
 305 310 315 320
 Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
 325 330 335
 Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
 340 345 350
 Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
 355 360 365
 Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
 370 375 380
 Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
 385 390 395 400
 Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
 405 410 415
 Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
 420 425 430
 Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
 435 440 445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
 450 455 460
 Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
 465 470 475 480
 Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
 485 490 495
 Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
 500 505 510
 Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
 515 520 525
 Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
 530 535 540
 Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr
 545 550 555 560
 Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu
 565 570 575
 Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
 580 585 590
 Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
 595 600 605
 Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
 610 615 620
 Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
 625 630 635 640
 Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
 645 650 655
 Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
 660 665 670
 Arg Tyr Val Ile Leu Arg Met
 675

<210> 124
 <211> 2916
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (81)..(2117)

<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113
Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala
1 5 10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161
Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu
15 20 25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209
Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp
30 35 40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257
Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu
45 50 55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305
Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val
60 65 70 75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353
Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp
80 85 90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401
Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val
95 100 105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449
Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu
110 115 120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497
Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly
125 130 135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545
Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu
140 145 150 155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593
Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile
160 165 170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys
175 180 185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala
190 195 200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg 737
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro
205 210 215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg	785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser	
220 225 230 235	
gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt	833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys	
240 245 250	
ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct	881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser	
255 260 265	
gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa	929
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu	
270 275 280	
gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct	977
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser	
285 290 295	
gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga	1025
Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg	
300 305 310 315	
aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag	1073
Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu	
320 325 330	
agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc	1121
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr	
335 340 345	
gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt	1169
Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser	
350 355 360	
caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac	1217
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His	
365 370 375	
acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta	1265
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu	
380 385 390 395	
cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc	1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro	
400 405 410	
tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc	1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly	
415 420 425	
atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa	1409
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu	
430 435 440	

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457
 Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile
 445 450 455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505
 Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His
 460 465 470 475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553
 Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly
 480 485 490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601
 Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp
 495 500 505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649
 Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala
 510 515 520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697
 Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile
 525 530 535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745
 Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser
 540 545 550 555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt 1793
 Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly
 560 565 570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg 1841
 Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met
 575 580 585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa 1889
 Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu
 590 595 600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc 1937
 Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro
 605 610 615

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg 1985
 Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp
 620 625 630 635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033
 Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe
 640 645 650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081
 Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala
 655 660 665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctggt 2127

Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met
 670 675

tgagattaaa atttgtgtca atgtttggga ccatottagg tattcctgct cccctgaaga 2187
 atgattacag tgtaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247
 aagtgttact tgtgtcataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307
 tgtaaaatag cccgggttcc actggctcct gctgagggtcc cctttccttc tgggctgtga 2367
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 aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607
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 gatgagggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727
 tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787
 ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847
 ttaaattggga cagccttcca tgttcatttg tctacctott aactgaataa aaaagcctac 2907
 agtttttag 2916

<210> 125
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 125
 Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala
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 Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu
 20 25 30
 Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys
 35 40 45
 Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
 50 55 60
 Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
 65 70 75 80
 Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
 85 90 95
 Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln

100

105

110

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
115 120 125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
130 135 140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145 150 155 160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
165 170 175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
180 185 190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
195 200 205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
210 215 220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225 230 235 240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
245 250 255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
260 265 270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
275 280 285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(944)

<400> 126

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acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113
Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln
1 5 10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161
Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln
15 20 25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr
 30 35 40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257
 Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val
 45 50 55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305
 Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala
 60 65 70 75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353
 Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln
 80 85 90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401
 Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr
 95 100 105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449
 Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg
 110 115 120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497
 Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly
 125 130 135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545
 Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu
 140 145 150 155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593
 Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn
 160 165 170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641
 Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn
 175 180 185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689
 Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala
 190 195 200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737
 Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu
 205 210 215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785
 Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly
 220 225 230 235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833
 Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu
 240 245 250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881
 Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929
 Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val
 270 275 280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984
 Gly Leu Tyr Ala Met
 285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggcttcct taccgtgggc 1044
 actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104
 ggagcctatg gcattctccc caacgaaaag cacatccagg caatggccta aacttcagag 1164
 ggggcgaagg ggtcagccct gcccttcage atcctcagtt cctgcagcag agcctggaag 1224
 acacccta at gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284
 tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344
 atgttggtgc ttgtgttttt gtcttatttt tggtggagcc actctgttcc tggctcagcc 1404
 tcaa atgcag tatttttgtt gtgttctggt gtttttatag caggggtggg gtgggttttg 1464
 agccatgcgt ggggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524
 tgtgaaataa taaacaacat tgtctg 1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu
 1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val
 20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro
 35 40 45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
 50 55 60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe
 65 70 75 80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn
 85 90 95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg
 100 105 110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys
 115 120 125

Ile Lys Cys Val Ala Phe Asp
 130 135

<210> 128
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(454)

<400> 128
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 Met Ala Cys
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ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106
 Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
 5 10 15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154
 Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
 20 25 30 35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202
 Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
 40 45 50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250
 Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
 55 60 65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
 Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
 70 75 80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
 Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
 85 90 95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
 Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
 100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442
 Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
 120 125 130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494
 Val Ala Phe Asp
 135

ctctgctccc ctg

<210> 129
 <211> 662
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn
 1 5 10 15
 Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn
 20 25 30
 Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp
 35 40 45
 Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys
 50 55 60
 Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser
 65 70 75 80
 Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr
 85 90 95
 Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu
 100 105 110
 Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys
 115 120 125
 His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
 130 135 140
 Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
 145 150 155 160
 Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
 165 170 175
 Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
 180 185 190
 Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
 195 200 205
 Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
 210 215 220
 Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
 225 230 235 240
 Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
 245 250 255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
 260 265 270
 Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
 275 280 285
 Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
 290 295 300
 Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
 305 310 315 320
 Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
 325 330 335
 Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
 340 345 350
 Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
 355 360 365
 Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln
 370 375 380
 Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp
 385 390 395 400
 Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
 405 410 415
 Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
 420 425 430
 Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
 435 440 445
 Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
 450 455 460
 Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
 465 470 475 480
 Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
 485 490 495
 Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
 500 505 510
 Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
 515 520 525
 Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn
 530 535 540
 Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
 545 550 555 560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln
565 570 575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln
580 585 590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn
595 600 605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe
610 615 620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn
625 630 635 640

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Leu Arg Ile Ser Glu Lys
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Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu
1 5 10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157
Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys
15 20 25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205
Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu
30 35 40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253
Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val
45 50 55 60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301
Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu
65 70 75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349
Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397
 Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu
 95 100 105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445
 Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly
 110 115 120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493
 Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys
 125 130 135 140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541
 Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr
 145 150 155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589
 Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr
 160 165 170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637
 Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn
 175 180 185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685
 Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val
 190 195 200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733
 Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser
 205 210 215 220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781
 Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe
 225 230 235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829
 Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly
 240 245 250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877
 His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala
 255 260 265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925
 Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu
 270 275 280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973
 Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
 285 290 295 300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021
 Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
 305 310 315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069
 Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln
 320 325 330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117
 Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile
 335 340 345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165
 Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr
 350 355 360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213
 Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr
 365 370 375 380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261
 Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg
 385 390 395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309
 Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu
 400 405 410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357
 Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met
 415 420 425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405
 Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala
 430 435 440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453
 Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro
 445 450 455 460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501
 Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp
 465 470 475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549
 Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr
 480 485 490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597
 Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr
 495 500 505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645
 Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val
 510 515 520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693
 Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys
 525 530 535 540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741
 Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His 555
 545

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789
 Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn 570
 560

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837
 Gly Pro Tyr Gln Ser Ser Ala Thr Ser Gly Gly Ala Gly His Tyr 585
 575

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885
 His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly 600
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aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933
 Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr 620
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cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981
 Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe 635
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agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029
 Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser 650
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ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079
 Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys 660
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gtagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

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<211> 824

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<213> Homo sapiens

<400> 131

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Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala 45
 35 40

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg 60
 50 55

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys 80
 65 70 75

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met 95
 85 90

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala 110
 100 105

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys 125
 115 120

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val 140
 130 135

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp 160
 145 150 155

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile 175
 165 170

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val 190
 180 185

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val 205
 195 200

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu 220
 210 215

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro 240
 225 230 235

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro 255
 245 250

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys 270
 260 265

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr 285
 275 280

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val 300
 290 295

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp 320
 305 310 315

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp 335
 325 330

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn 350
 340 345

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu 365
 355 360

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
 370 380
 Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
 385 390 395 400
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 405 410 415
 Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
 420 425 430
 Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
 435 440 445
 Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
 450 455 460
 Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
 465 470 475 480
 Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
 485 490 495
 Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
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 515 520 525
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 530 535 540
 Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
 545 550 555 560
 Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
 565 570 575
 Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
 580 585 590
 Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
 595 600 605
 Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
 610 615 620
 Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
 625 630 635 640
 Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
 645 650 655
 Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
 660 665 670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
675 680 685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
690 695 700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705 710 715 720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
725 730 735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
740 745 750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
755 760 765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
770 775 780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
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<213> Homo sapiens

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gggcgggscg gagccccggc agtccggggt cgccggcgag ggcc atg tcg ctg ttg 176
Met Ser Leu Leu

1

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Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro
5 10 15 20

ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272
Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro
25 30 35

ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg 320
 Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg
 40 45 50

ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368
 Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg
 55 60 65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416
 Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro
 70 75 80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464
 Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly
 85 90 95 100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512
 Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr
 105 110 115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560
 Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn
 120 125 130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608
 Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys
 135 140 145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656
 Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn
 150 155 160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704
 Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val
 165 170 175 180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc 752
 His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe
 185 190 195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca 800
 Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro
 200 205 210

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848
 Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln
 215 220 225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896
 Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu
 230 235 240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944
 Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp
 245 250 255 260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992

Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met 275
 265 270

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040
 Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val 290
 280 285

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088
 Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile 305
 295 300

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136
 Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn 320
 310 315

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg 1184
 Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala 340
 325 330 335

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232
 Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His 355
 345 350

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280
 Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu 370
 360 365

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa 1328
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 375 380

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag 1376
 Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Asp Lys 400
 390 395

gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt 1424
 Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe 420
 405 410 415

ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct 1472
 Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser 435
 425 430

gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa 1520
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 440 445

gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat 1568
 Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn 465
 455 460

gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc 1616
 Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala 480
 470 475

aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa 1664
 Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu

485

490

495

500

atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa 1712
 Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys
 505 510 515

gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt 1760
 Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val
 520 525 530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808
 Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu
 535 540 545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856
 Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile
 550 555 560

cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg 1904
 Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp
 565 570 575 580

gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt 1952
 Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys
 585 590 595

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 Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met
 600 605 610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt 2048
 Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys
 615 620 625

gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa 2096
 Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys
 630 635 640

gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca 2144
 Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser
 645 650 655 660

aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa 2192
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 665 670 675

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240
 Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
 680 685 690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288
 Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly
 695 700 705

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 Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
 710 715 720

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 725 730 735 740
 gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432
 Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
 745 750 755
 ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca 2480
 Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
 760 765 770
 cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca 2528
 Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
 775 780 785
 agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca 2576
 Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
 790 795 800
 gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624
 Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
 805 810 815 820
 att tct gaa aaa tgacctcctt gtttttgaaa gtttagcataa ttttagatgc 2676
 Ile Ser Glu Lys
 ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736
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 <212> PRT
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 35 40 45
 Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp
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 Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys
 65 70 75 80
 Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile
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Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu
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Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu
130 135 140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr
145 150 155 160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe
165 170 175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr
180 185 190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly
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Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg
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Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu
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Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr
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Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr
260 265 270

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly
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Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala
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Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu
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Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro
325 330 335

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340 345 350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
355 360 365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly
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Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala

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Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
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Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
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Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
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Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
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Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
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530 535 540

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Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His
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Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala
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Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp
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245

690

695

700

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Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp
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755 760 765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile
770 775 780

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785 790 795 800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val
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820 825 830

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835 840 845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu
850 855 860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe
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Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu
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Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu
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Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile
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Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys
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Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val
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cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900
Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly
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gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc 948
Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg
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 Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro
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cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668
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405

410

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 Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln
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gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100
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 Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln
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 Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro
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agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt 2340
 Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val
 625 630 635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct 2388
 Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala
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gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa 2436
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 655 660 665 670

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 Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe
 690 695 700

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 720 725 730

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga 2676
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 735 740 745 750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724
 Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp
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aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772
 Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
 770 775 780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820
 Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
 785 790 795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868
 Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
 800 805 810

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 Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
 815 820 825 830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964
 Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
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 Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu
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 895 900 905 910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt 3203
 Ser Thr Ser Ser Ser Phe Leu Glu Val
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 35 40 45
 Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly
 50 55 60
 Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr
 65 70 75 80
 Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn
 85 90 95
 Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met
 100 105 110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr
 115 120 125
 Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys
 130 135 140
 Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe
 145 150 155 160
 Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln
 165 170 175
 Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala
 180 185 190
 Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys
 195 200 205
 Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile
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 Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly
 225 230 235 240
 Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser
 245 250 255
 Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val
 260 265 270
 Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu
 275 280 285
 Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys
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 Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile
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 Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr
 325 330 335
 Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala
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cgggggcccg gacgcagccc ggctcctccc ctctccgcc ccttccccag cctgacctgg 300

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 Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala
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tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665
 Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His
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Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly
75 80 85 90

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809
Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala
110 115 120

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905

Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn
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agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953
 Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu
 155 160 165 170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001
 Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg
 175 180 185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049
 Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr
 190 195 200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097
 Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu
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cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145
 Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile
 220 225 230

atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc 1193
 Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu
 235 240 245 250

tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241
 Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys
 255 260 265

gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac 1289
 Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp
 270 275 280

aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg 1337
 Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser
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cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc 1385
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aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta 1433
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 315 320 325 330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481
 Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro
 335 340 345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529
 Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr
 350 355 360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577
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 Asp Asp Met Trp
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 agccagtccc ttcatttaac tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229
 caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289
 ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349
 tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttcta 2409
 gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137
 <211> 358
 <212> PRT
 <213> Homo sapiens

<400> 137
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 20 25 30
 Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu
 35 40 45
 Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val
 50 55 60
 Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg
 65 70 75 80
 Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
 100 105 110
 Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
 115 120 125
 Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
 130 135 140
 Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
 145 150 155 160
 Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
 165 170 175
 Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
 180 185 190
 Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
 195 200 205
 Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
 210 215 220
 Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
 225 230 235 240
 Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
 245 250 255
 Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln
 260 265 270
 Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr
 275 280 285
 Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln
 290 295 300
 Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly
 305 310 315 320
 Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro
 325 330 335
 Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln
 340 345 350
 Pro Gly Pro Gly Tyr Arg
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<210> 138
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 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

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gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca      97
Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr
      15              20              25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata      145
Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile
      30              35              40              45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca      193
Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser
            50              55              60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa      241
Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys
            65              70              75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct      289
Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro
            80              85              90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag      337
Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
            95              100              105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca      385
Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
      110              115              120              125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa      433
Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
            130              135              140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca      481
Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
            145              150              155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct      529
Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala
            160              165              170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca      577
Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
            175              180              185

cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac      625
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
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190

195

200

205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673
 Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
 210 215 220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag 721
 Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
 225 230 235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca 769
 Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
 240 245 250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg 817
 Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
 255 260 265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa 865
 Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
 270 275 280 285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913
 Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
 290 295 300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961
 Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
 305 310 315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009
 Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
 320 325 330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag gcc 1057
 Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly
 335 340 345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104
 Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
 350 355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag cattttttat gatattcattg ttggtgttaa 1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tcctgctta 1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga 1344

cttgactttc tagcttcct tgtccggagg atattaaaat gctaggggtga ggttttagcca 1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

gatattatgt ataaaatgta aactgatga taggttaata aagatgattg aatcc 1519

<210> 139
<211> 396
<212> PRT
<213> Homo sapiens

<400> 139
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Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr
20 25 30
Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu
35 40 45
Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp
50 55 60
Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys
65 70 75 80
Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro
85 90 95
Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
100 105 110
Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
115 120 125
Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
130 135 140
Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145 150 155 160
Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
165 170 175
Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
180 185 190
Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
195 200 205
Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
210 215 220
Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225 230 235 240
Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
245 250 255
Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
260 265 270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
275 280 285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
290 295 300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
305 310 315 320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
325 330 335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
355 360 365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
370 375 380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
385 390 395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140
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1 5 10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99
Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His
15 20 25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147
Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val
30 35 40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195
Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys
45 50 55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243
Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser
60 65 70 75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291
Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn
260

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339
 Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg
 95 100 105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387
 Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu
 110 115 120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435
 Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp
 125 130 135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483
 Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys
 140 145 150 155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531
 Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu
 160 165 170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579
 Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu
 175 180 185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627
 Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg
 190 195 200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca 675
 Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro
 205 210 215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa 723
 Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln
 220 225 230 235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca 771
 Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala
 240 245 250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819
 Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln
 255 260 265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867
 Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln
 270 275 280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915
 Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
 285 290 295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963
 Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
 300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011
 Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
 320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059
 Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
 335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107
 Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro
 350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155
 Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg
 365 370 375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203
 Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr
 380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256
 Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316
 cattttttat gatatacattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376
 ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436
 acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg 1496
 atattaaaat gctaggggtga ggttttagcca tcttacttgg ctttttacta ttaacatgat 1556
 gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616
 taggttaata aagatgattg aatcc 1641

<210> 141
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 141
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Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn
 35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
 50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
 65 70 75 80
 Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
 85 90 95
 Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
 100 105 110
 Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
 115 120 125
 His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
 130 135 140
 Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
 145 150 155 160
 Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
 165 170 175
 Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
 180 185 190
 Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
 195 200 205
 Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
 210 215 220
 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
 225 230 235 240
 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
 245 250 255
 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
 260 265 270
 Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
 275 280 285
 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
 290 295 300
 Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
 305 310 315 320
 Val Gln Thr

<210> 142
 <211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72)..(1040)

<400> 142
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gcggcgagaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110
 Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro
 1 5 10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158
 Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu
 15 20 25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206
 Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe
 30 35 40 45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254
 Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His
 50 55 60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302
 Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg
 65 70 75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350
 Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe
 80 85 90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398
 Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
 95 100 105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446
 Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
 110 115 120 125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
 Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
 130 135 140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
 Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
 145 150 155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
 Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
 160 165 170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
 Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
 175 180 185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686
 Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

190

195

200

205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734
 Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg
 210 215 220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782
 Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn
 225 230 235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830
 Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn
 240 245 250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878
 Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val
 255 260 265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926
 Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu
 270 275 280 285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974
 Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu
 290 295 300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022
 Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln
 305 310 315

ctg acc cat gtg cag aca taggcggcctt cctggccctg gggccggggg 1070
 Leu Thr His Val Gln Thr
 320

ctgggggtgtg gggcagctctg ggctcctctca tcatccccac ttcccaggcc cagcctttcc 1130
 aacctgcct gggatctggg ctttaatgca gaggccatgt ccttgtcttg tctgtcttct 1190
 ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250
 cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310
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 gcagctccac ccagtcacca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc 1430
 agcccctcct ctctgacctt taacctcact ctcaccttgc accgtgcacc aaccttcac 1490
 ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550
 ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610
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<210> 143

<211> 136

<212> PRT
<213> Homo sapiens

<400> 143
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Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
20 25 30
Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45
Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60
Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80
Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95
Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His
100 105 110
Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe
115 120 125
Leu Gln Pro Leu Met His Cys Val
130 135

<210> 144
<211> 1252
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (225)..(632)

<400> 144
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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180
aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
Met Ala Gly Ala
1
att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
5 10 15 20
ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
 25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
 Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
 40 45 50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
 Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
 55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
 Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
 70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctg ccc cac 524
 Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
 85 90 95 100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572
 Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser
 105 110 115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620
 Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu
 120 125 130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672
 Met His Cys Val
 135

ttgttaatta gtgacatagt aacatctgta gcagctggtt agtaaaccctc atgtgggggt 732
 ggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac 792
 atttttcttg ttttaaattc taggatagat tttaacatcc tttgcgggtcc cagtccaagg 852
 taggctggtg tcatagtctt ctcaactccta atccatgacc actgtttttt tcttatttat 912
 atcaccaggt agcctactga gttaatatatt aagttgtcaa tagataagtg tccctgtttt 972
 gtggcataat ataactgaat ttcattgagaa gattttattcc accaggggta tttcagcttt 1032
 gaaaccaaatt ctgtgtatct aataactaacc aatctgttgg atgtgggttt taaaaaatgt 1092
 ttgctaaact acccaagtaa gattttactgt attaaatggc cttcgggtct gaaaagcttt 1152
 tttaacctct tgcttaaaat gcgtttttatt ttgataagat acttcaaata gcctccaaaa 1212
 gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

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Pro	Ile	Ile	Val	Thr	Arg	Ser	Glu	Thr	Leu	Lys	Arg	Gln	Phe	Gln	Phe	
			20					25					30			
Met	Leu	Phe	Ile	Leu	Gln	Leu	Asp	Ile	Ala	Phe	Lys	Leu	Asn	Asn	Gln	
		35					40					45				
Ile	Arg	Glu	Asn	Ala	Glu	Val	Ser	Met	Asp	Val	Ser	Leu	Ala	Tyr	Arg	
	50					55					60					
Asp	Asp	Ala	Phe	Ala	Glu	Trp	Thr	Glu	Met	Ala	His	Glu	Arg	Val	Pro	
65					70					75					80	
Arg	Lys	Leu	Lys	Cys	Thr	Phe	Thr	Ser	Pro	Lys	Thr	Pro	Glu	His	Glu	
				85					90					95		
Gly	Arg	Tyr	Tyr	Glu	Cys	Asp	Val	Leu	Pro	Phe	Met	Glu	Ile	Gly	Ser	
		100						105					110			
Val	Ala	His	Lys	Phe	Tyr	Leu	Leu	Asn	Ile	Arg	Leu	Pro	Val	Asn	Glu	
		115						120					125			
Lys	Lys	Lys	Ile	Asn	Val	Gly	Ile	Gly	Glu	Ile	Lys	Asp	Ile	Arg	Leu	
	130					135						140				
Val	Gly	Ile	His	Gln	Asn	Gly	Gly	Phe	Thr	Lys	Val	Trp	Phe	Ala	Met	
145					150					155					160	
Lys	Thr	Phe	Leu	Thr	Pro	Ser	Ile	Phe	Ile	Ile	Met	Val	Trp	Tyr	Trp	
			165						170					175		
Arg	Arg	Ile	Thr	Met	Met	Ser	Arg	Pro	Pro	Val	Leu	Leu	Glu	Lys	Val	
			180					185					190			
Ile	Phe	Ala	Leu	Gly	Ile	Ser	Met	Thr	Phe	Ile	Asn	Ile	Pro	Val	Glu	
		195					200					205				
Trp	Phe	Ser	Ile	Gly	Phe	Asp	Trp	Thr	Trp	Met	Leu	Leu	Phe	Gly	Asp	
	210					215					220					
Ile	Arg	Gln	Gly	Ile	Phe	Tyr	Ala	Met	Leu	Leu	Ser	Phe	Trp	Ile	Ile	
225				230						235					240	
Phe	Cys	Gly	Glu	His	Met	Met	Asp	Gln	His	Glu	Arg	Asn	His	Ile	Ala	
			245						250					255		
Gly	Tyr	Trp	Lys	Gln	Val	Gly	Pro	Ile	Ala	Val	Gly	Ser	Phe	Cys	Leu	
			260					265					270			
Phe	Ile	Phe	Asp	Met	Cys	Glu	Arg	Gly	Val	Gln	Leu	Thr	Asn	Pro	Phe	
		275					280					285				
Tyr	Ser	Ile	Trp	Thr	Thr	Asp	Ile	Gly	Thr	Glu	Leu	Ala	Met	Ala	Phe	
	290					295					300					

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
 305 310 315 320
 Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
 325 330 335
 Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
 340 345 350
 Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
 355 360 365
 Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
 370 375 380
 Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
 385 390 395 400
 Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
 405 410 415
 Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
 420 425 430
 Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
 435 440 445
 Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
 450 455 460
 Ala Ser Gly Ile
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<210> 146
 <211> 1943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (379)..(1782)

<400> 146
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 cccagaaagg aggcgaggaa ggaggaggatg tgtgagagga gggagcaaaa agctcaccct 180
 aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240
 tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300
 tcatcgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgctcggtgaa atgtgtgg	atg ccc gta aga acc atc aca aga caa aat ggt	411
	Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly	
	1 5 10	
tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag	459	
Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys		
	15 20 25	
agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc	507	
Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe		
	30 35 40	
aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt	555	
Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val		
	45 50 55	
tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc	603	
Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala		
	60 65 70 75	
cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag	651	
His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys		
	80 85 90	
act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc	699	
Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe		
	95 100 105	
atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg	747	
Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg		
	110 115 120	
ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata	795	
Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile		
	125 130 135	
aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag	843	
Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys		
	140 145 150 155	
gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att	891	
Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile		
	160 165 170	
atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg	939	
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val		
	175 180 185	
ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc	987	
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile		
	190 195 200	
aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg	1035	
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met		
	205 210 215	
ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg	1083	

Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu	
220 225 230 235	
tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag	1131
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu	
240 245 250	
cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt	1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val	
255 260 265	
ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa	1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln	
270 275 280	
ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag	1275
Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu	
285 290 295	
ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac	1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr	
300 305 310 315	
ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt	1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser	
320 325 330	
ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac	1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His	
335 340 345	
tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg	1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu	
350 355 360	
gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg	1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr	
365 370 375	
gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc	1563
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala	
380 385 390 395	
ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg	1611
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu	
400 405 410	
atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc	1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser	
415 420 425	
aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt	1707
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe	
430 435 440	
gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc	1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe	

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802
 Ile Asn Asp Asn Ala Ala Ser Gly Ile
 460 465

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaata ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t 1943

<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
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Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly
 20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
 35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
 50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
 65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
 85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
 100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
 115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
 130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
 145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
 165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
 180 185 190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
 195 200 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
 210 215 220
 Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
 225 230 235 240
 Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
 245 250 255
 Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
 260 265 270
 Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
 275 280 285
 Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
 290 295 300
 Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg
 305 310 315 320
 Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg
 325 330 335
 Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu
 340 345 350
 Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser
 355 360 365
 Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val
 370 375 380
 Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val
 385 390 395 400
 Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
 405 410 415
 Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
 420 425 430
 Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
 435 440 445
 Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
 450 455 460

<210> 148
 <211> 1919
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (376)..(1755)

<400> 148

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gccttccgtc ccgggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120
agaaaggagg cgaggaagga gggagtgtat gagaggagg agcaaaaagc tcaccctaaa 180
acatttattt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240
aaaacatgag caccaagaag ctgtgcattg ttgggtgggat tctgctcgtg ttccaaatca 300
tcgcctttct ggtgggaggc ttgattgctc cagggcccac aacggcagtg tcctacatgt 360
cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411
      Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser
      1             5             10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459
Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg
      15             20             25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507
Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr
      30             35             40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555
Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe
      45             50             55

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603
Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys
      65             70             75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651
Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr
      80             85             90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699
Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys
      95             100             105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747
Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
      110             115             120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795
Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
      125             130             135

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
      145             150             155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
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160

165

170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939
 Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
 175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987
 Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile
 190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag gcc 1035
 Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly
 205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083
 Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu
 225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131
 His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys
 240 245 250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179
 Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp
 255 260 265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227
 Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp
 270 275 280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275
 Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala
 285 290 295 300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323
 Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe
 305 310 315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg 1371
 Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met
 320 325 330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419
 Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys
 335 340 345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467
 Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe
 350 355 360

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515
 Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
 365 370 375 380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
 Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
 385 390 395

275

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
 Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
 400 405 410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
 Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
 415 420 425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707
 Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
 430 435 440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755
 Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
 445 450 455 460

tgagtcaaca aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaatt 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc 1919

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
 130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175

Asp Arg His Lys Met Leu Ser
 180

<210> 150
 <211> 1562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (120)..(668)

<400> 150
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 ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119
 atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1 5 10 15
 cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30
 tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45
 tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60
 cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80
 gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95
 tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110
 gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125
 gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
 130 135 140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698
 Asp Arg His Lys Met Leu Ser
 180

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aggtgtgctgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggtttcatt 180
ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230
Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly
1 5 10
att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278
Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys
15 20 25
ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326
Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala
30 35 40 45
atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374
Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu
50 55 60
gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422
Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp
65 70 75
gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470
Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser
80 85 90
tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518
Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys
95 100 105
ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566
Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe
110 115 120 125
gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614
Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp
130 135 140
gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662
Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro
145 150 155
ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710
Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala
160 165 170
gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758
Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp
175 180 185
gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806
Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His
190 195 200 205

cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat	854
Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His	
210 215 220	
gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag	902
Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln	
225 230 235	
gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc	950
Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser	
240 245 250	
tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa	998
Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu	
255 260 265	
att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct	1046
Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro	
270 275 280 285	
gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc	1094
Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys	
290 295 300	
aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa	1142
Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu	
305 310 315	
agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt	1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val	
320 325 330	
cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct	1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro	
335 340 345	
gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct	1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro	
350 355 360 365	
ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc	1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser	
370 375 380	
aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat	1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr	
385 390 395	
aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt	1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg	
400 405 410	
att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc	1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe	
415 420 425	
tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa	1526

Cys	Glu	Glu	Phe	Gln	Val	Pro	Gly	Arg	Gly	Glu	Leu	His	Cys	Leu	Gln	
430					435					440					445	
gat	gcc	atc	gat	cac	tcg	ggg	ttc	acg	atc	ctg	ctc	ctg	act	gct	agc	1574
Asp	Ala	Ile	Asp	His	Ser	Gly	Phe	Thr	Ile	Leu	Leu	Leu	Thr	Ala	Ser	
				450					455					460		
ttt	gat	tgc	agc	ctg	agc	ctg	cat	caa	atc	aac	cat	gct	ctc	atg	aac	1622
Phe	Asp	Cys	Ser	Leu	Ser	Leu	His	Gln	Ile	Asn	His	Ala	Leu	Met	Asn	
			465					470					475			
agc	ctt	aca	cag	tct	ggg	agg	cag	gac	tgt	gtg	atc	ccc	ctc	ctc	cca	1670
Ser	Leu	Thr	Gln	Ser	Gly	Arg	Gln	Asp	Cys	Val	Ile	Pro	Leu	Leu	Pro	
		480					485					490				
ctt	gag	tgt	tcc	cag	gcc	cag	ctc	agc	cca	gat	aca	acc	aga	ctg	ctc	1718
Leu	Glu	Cys	Ser	Gln	Ala	Gln	Leu	Ser	Pro	Asp	Thr	Thr	Arg	Leu	Leu	
	495					500					505					
cac	agc	att	gtg	tgg	ctg	gat	gaa	cac	tcc	cca	atc	ttc	gcc	aga	aag	1766
His	Ser	Ile	Val	Trp	Leu	Asp	Glu	His	Ser	Pro	Ile	Phe	Ala	Arg	Lys	
510					515					520					525	
gtg	gca	aac	acc	ttc	aag	aca	cag	aag	ctc	cag	gca	cag	cgg	gta	cgc	1814
Val	Ala	Asn	Thr	Phe	Lys	Thr	Gln	Lys	Leu	Gln	Ala	Gln	Arg	Val	Arg	
				530					535					540		
tgg	aag	aaa	gcg	cag	gag	gcc	aga	acc	ctc	aag	gag	cag	agc	ata	cag	1862
Trp	Lys	Lys	Ala	Gln	Glu	Ala	Arg	Thr	Leu	Lys	Glu	Gln	Ser	Ile	Gln	
			545					550					555			
ctg	gag	gca	gag	cgg	caa	aac	gtg	gca	gcc	ata	tct	gct	gcc	tac	aca	1910
Leu	Glu	Ala	Glu	Arg	Gln	Asn	Val	Ala	Ala	Ile	Ser	Ala	Ala	Tyr	Thr	
		560					565					570				
gcc	tat	gtc	cat	agc	tat	agg	gcc	tgg	caa	gca	gag	atg	aac	aaa	ctt	1958
Ala	Tyr	Val	His	Ser	Tyr	Arg	Ala	Trp	Gln	Ala	Glu	Met	Asn	Lys	Leu	
	575					580					585					
ggg	gtg	gct	ttt	ggg	aag	aac	ttg	tca	ctg	ggg	act	cca	aca	ccc	agc	2006
Gly	Val	Ala	Phe	Gly	Lys	Asn	Leu	Ser	Leu	Gly	Thr	Pro	Thr	Pro	Ser	
590					595					600					605	
tgg	ccc	gga	tgt	cca	cag	cca	ata	cct	tct	cat	cct	cag	ggt	ggt	act	2054
Trp	Pro	Gly	Cys	Pro	Gln	Pro	Ile	Pro	Ser	His	Pro	Gln	Gly	Gly	Thr	
				610					615					620		
cca	gtt	ttc	ccc	tat	tcc	cca	cag	cct	cca	tcc	ttc	cct	cag	cct	cca	2102
Pro	Val	Phe	Pro	Tyr	Ser	Pro	Gln	Pro	Pro	Ser	Phe	Pro	Gln	Pro	Pro	
			625					630					635			
tgc	ttc	cct	cag	cct	cca	tcc	ttc	cct	cag	cct	cca	tcc	ttc	cca	ctg	2150
Cys	Phe	Pro	Gln	Pro	Pro	Ser	Phe	Pro	Gln	Pro	Pro	Ser	Phe	Pro	Leu	
		640					645					650				
cct	cca	gtc	tct	tcc	cca	cag	tcc	caa	tcc	ttt	cca	tca	gcc	tcc	tcc	2198
Pro	Pro	Val	Ser	Ser	Pro	Gln	Ser	Gln	Ser	Phe	Pro	Ser	Ala	Ser	Ser	

655

660

665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc 2246
 Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala
 670 675 680 685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg 2294
 Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly
 690 695 700

gcc cag tca tct gat gac aag act gag tgt tgc gag aac ccc tgt atg 2342
 Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met
 705 710 715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag 2387
 Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
 720 725 730

tgaccaggtt ggacccacc tagatggcta gagtgacaag attggacttc acctgggtcc 2447
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 gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca tagggctctt 2747
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<211> 732

<212> PRT

<213> Homo sapiens

<400> 152

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 20 25 30

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu
 35 40 45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu
 50 55 60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met
 65 70 75 80

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser
100 105 110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln
115 120 125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys
130 135 140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser
145 150 155 160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg
165 170 175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr
180 185 190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile
195 200 205

Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His
210 215 220

Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln
225 230 235 240

Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro
245 250 255

Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val
260 265 270

Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu
275 280 285

Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu
290 295 300

Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly
305 310 315 320

Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly
325 330 335

Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro
340 345 350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser
355 360 365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro
370 375 380

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val

385	390	395	400
Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu	405	410	415
Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu	420	425	430
Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile	435	440	445
Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys	450	455	460
Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr	465	470	475
Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys	485	490	495
Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile	500	505	510
Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn	515	520	525
Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys	530	535	540
Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala	545	550	555
Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val	565	570	575
His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala	580	585	590
Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly	595	600	605
Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe	610	615	620
Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro	625	630	635
Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val	645	650	655
Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro	660	665	670
Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val	675	680	685
Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser			

690

695

700

Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu
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Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
725 730

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Met Ala Cys Thr Gly Pro
1 5
tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag 162
Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys
10 15 20
ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210
Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln
25 30 35
ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258
Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu
40 45 50
act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306
Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala
55 60 65 70
cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354
Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro
75 80 85
gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402
Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu
90 95 100
ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450
Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr
105 110 115
cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498
Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly
120 125 130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg	546
Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly	
135 140 145 150	
gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca	594
Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro	
155 160 165	
cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att	642
Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile	
170 175 180	
gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc	690
Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly	
185 190 195	
agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc	738
Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr	
200 205 210	
atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc	786
Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu	
215 220 225 230	
tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc	834
Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly	
235 240 245	
tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc	882
Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala	
250 255 260	
agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg	930
Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val	
265 270 275	
gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca	978
Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro	
280 285 290	
gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc	1026
Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly	
295 300 305 310	
ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc	1074
Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys	
315 320 325	
tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc	1122
Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr	
330 335 340	
tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca	1170
Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Pro Pro Glu Thr	
345 350 355	

tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct	1218
Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala	
360 365 370	
cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg	1266
His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser	
375 380 385 390	
gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa	1314
Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu	
395 400 405	
cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc	1362
His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro	
410 415 420	
gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag	1410
Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu	
425 430 435	
ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta	1458
Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu	
440 445 450	
ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac	1506
Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn	
455 460 465 470	
caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc	1554
Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val	
475 480 485	
atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac	1602
Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp	
490 495 500	
acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag	1650
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln	
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atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag	1698
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln	
520 525 530	
gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg	1746
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg	
535 540 545 550	
gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg	1794
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu	
555 560 565	
aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca	1842
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala	
570 575 580	
cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg	1890

Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly
 585 590 595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc 1938
 Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro
 600 605 610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg 1986
 Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro
 615 620 625 630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca 2034
 Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro
 635 640 645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc 2082
 Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala
 650 655 660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc 2130
 Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro
 665 670 675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178
 Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His
 680 685 690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226
 Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
 695 700 705 710

gca gaa tgaccgcgtg tccttgccctg accacctggg gaacacccct ggacccaggc 2282
 Ala Glu

atcggccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat 2342

gaggatcatct gccactttca ggacattgtc cgggagccct tcatttagga caaacgggc 2402

gcgatgatgc cctggctttc aggggtggtca gaactggata cggtgtttac aattccaatc 2462

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<212> PRT

<213> Homo sapiens

<400> 154

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 35 40 45
 Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu
 50 55 60
 Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
 65 70 75 80
 Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
 85 90 95
 Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
 100 105 110
 Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
 115 120 125
 Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
 130 135 140
 Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
 145 150 155 160
 Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
 165 170 175
 Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
 180 185 190
 Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
 195 200 205
 Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
 210 215 220
 His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
 225 230 235 240
 Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
 245 250 255
 Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro
 260 265 270
 Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
 275 280 285
 Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
 290 295 300
 Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
 305 310 315 320
 Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu
 325 330 335

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
 340 345 350
 Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser
 355 360 365
 Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
 370 375 380
 Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
 385 390 395 400
 His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
 405 410 415
 Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
 420 425 430
 Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
 435 440 445
 Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
 450 455 460
 Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
 465 470 475 480
 Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
 485 490 495
 Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
 500 505 510
 Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
 515 520 525
 Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
 530 535 540
 Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
 545 550 555 560
 Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
 565 570 575
 Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
 580 585 590
 Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
 595 600 605
 Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp
 610 615 620
 Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr
 625 630 635 640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro
645 650 655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
660 665 670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln
675 680 685

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Glu Asp Lys Thr Gln Glu Ala Glu
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ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa 180
gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240
tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca 295
Met Lys Lys Lys Ser
1 5
ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg 343
Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu
10 15 20
ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc 391
Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu
25 30 35
acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc 439
Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala
40 45 50
cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac 487
Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp
55 60 65
tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc 535
Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro

70	75	80	85	
ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac				583
Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp				
	90	95	100	
atc ttg gcc cct ggc cgc cgc cgc aag aac atg tgc gag ttc ctg ggg				631
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly				
	105	110	115	
gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct				679
Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser				
	120	125	130	
ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag				727
Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys				
	135	140	145	
aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc				775
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser				
	150	155	160	165
acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc				823
Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly				
	170	175	180	
aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg				871
Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly				
	185	190	195	
ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag				919
Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu				
	200	205	210	
gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc				967
Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu				
	215	220	225	
att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag				1015
Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu				
	230	235	240	245
gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg				1063
Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu				
	250	255	260	
cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag				1111
Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu				
	265	270	275	
tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc				1159
Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile				
	280	285	290	
cgg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg				1207
Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala				
	295	300	305	

ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly 310 315 320 325	1255
gac ttc ctc aaa ggc ttc aag atg ttc ggc tgc ctc ttc aag ccc tac Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr 330 335 340	1303
atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly 345 350 355	1351
ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu 360 365 370	1399
aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys 375 380 385	1447
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ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln 425 430 435	1591
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tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys 455 460 465	1687
gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro 470 475 480 485	1735
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ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu 505 510 515	1831
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agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac	1927
Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp	
535 540 545	
cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta	1975
Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val	
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ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg	2023
Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp	
570 575 580	
gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca	2071
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala	
585 590 595	
cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag	2119
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu	
600 605 610	
gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gaa	2167
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu	
615 620 625	
ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg	2215
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg	
630 635 640 645	
aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc	2263
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser	
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acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc	2311
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser	
665 670 675	
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Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr	
680 685 690	
tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg	2407
Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu	
695 700 705	
ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac	2455
Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr	
710 715 720 725	
ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca	2503
Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro	
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atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc	2551
Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser	
745 750 755	
cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg	2599

Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu
 760 765 770

agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc 2647
 Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu
 775 780 785

cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc 2695
 Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser
 790 795 800 805

cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg 2743
 Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg
 810 815 820

act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg 2791
 Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly
 825 830 835

gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg 2839
 Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly
 840 845 850

gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg 2887
 Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly
 855 860 865

gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag 2935
 Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Gly Val Ser Ala Gln
 870 875 880 885

cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg 2983
 His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu
 890 895 900

ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gagggcccca 3036
 Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
 905 910

agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc 3096

ttcagctact gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc 3156

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<210> 156
 <211> 912
 <212> PRT

<213> Homo sapiens

<400> 156

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			20					25					30		
Thr	Pro	Leu	Ser	Leu	Thr	Phe	Glu	Ala	Tyr	Arg	Phe	Gly	Gly	His	Tyr
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Leu	Arg	Val	Lys	Ala	Pro	Ala	Lys	Pro	Gly	Asp	Glu	Gly	Lys	Val	Glu
	50					55					60				
Gln	Gly	Met	Lys	Asp	Ser	Lys	Ser	Leu	Ser	Leu	Pro	Ile	Leu	Arg	Pro
65					70					75					80
Ala	Gly	Thr	Gly	Pro	Pro	Ala	Leu	Glu	Arg	Val	Asp	Ala	Gln	Ser	Arg
				85					90					95	
Arg	Glu	Ser	Leu	Asp	Ile	Leu	Ala	Pro	Gly	Arg	Arg	Arg	Lys	Asn	Met
			100					105					110		
Ser	Glu	Phe	Leu	Gly	Glu	Ala	Ser	Ile	Pro	Gly	Gln	Glu	Pro	Pro	Thr
		115					120					125			
Pro	Ser	Ser	Cys	Ser	Leu	Pro	Ser	Gly	Ser	Ser	Gly	Ser	Thr	Asn	Thr
	130					135					140				
Gly	Asp	Ser	Trp	Lys	Asn	Arg	Ala	Ala	Ser	Arg	Phe	Ser	Gly	Phe	Phe
145					150					155					160
Ser	Ser	Gly	Pro	Ser	Thr	Ser	Ala	Phe	Gly	Arg	Glu	Val	Asp	Lys	Met
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Glu	Gln	Leu	Glu	Gly	Lys	Leu	His	Thr	Tyr	Ser	Leu	Phe	Gly	Leu	Pro
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Arg	Leu	Pro	Arg	Gly	Leu	Arg	Phe	Asp	His	Asp	Ser	Trp	Glu	Glu	Glu
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Tyr	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Asn	Ala	Cys	Leu	Arg	Leu	Glu	Asp
	210					215					220				
Ser	Trp	Arg	Glu	Leu	Ile	Asp	Gly	His	Glu	Lys	Leu	Thr	Arg	Arg	Gln
225					230					235					240
Cys	His	Gln	Gln	Glu	Ala	Val	Trp	Glu	Leu	Leu	His	Thr	Glu	Ala	Ser
				245					250					255	
Tyr	Ile	Arg	Lys	Leu	Arg	Val	Ile	Ile	Asn	Leu	Phe	Leu	Cys	Cys	Leu
			260					265					270		
Leu	Asn	Leu	Gln	Glu	Ser	Gly	Leu	Leu	Cys	Glu	Val	Glu	Ala	Glu	Arg
		275					280					285			

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp
 290 295 300
 Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala
 305 310 315 320
 Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser
 325 330 335
 Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met
 340 345 350
 Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr
 355 360 365
 Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser
 370 375 380
 Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu
 385 390 395 400
 Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala
 405 410 415
 Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn
 420 425 430
 Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val
 435 440 445
 Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val
 450 455 460
 Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile
 465 470 475 480
 Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser
 485 490 495
 Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe
 500 505 510
 Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu
 515 520 525
 Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys
 530 535 540
 Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu
 545 550 555 560
 Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala
 565 570 575
 Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu
 580 585 590

Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln
 595 600 605
 Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu
 610 615 620
 Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser
 625 630 635 640
 Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
 645 650 655
 Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro
 660 665 670
 Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser
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 Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro
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 Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
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 Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val
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 Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg
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Leu	Leu	His	Thr	Glu	Ala	Ser	Tyr	Ile	Arg	Lys	Leu	Arg	Val	Ile	Ile					
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Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu	
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Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln	
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Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro	
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cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta	2668

Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu
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 Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser
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 Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro
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 His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala
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 Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
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 Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser
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 225 230 235 240
 Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser

245

250

255

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 Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr
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Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser
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Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val

850

855

860

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Met Gly Trp Lys Pro Ser Glu
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Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
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Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly	90	95	100	
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Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu	105	110	115	
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Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys	120	125	130	135
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Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys	155	160	165	
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His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg	170	175	180	
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Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg	185	190	195	
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Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp	200	205	210	215
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Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile	220	225	230	
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Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp	235	240	245	
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gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac	1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr	
425 430 435	
cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag	1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu	
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Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys	
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Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val	
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Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu	
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Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val	
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Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val	
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Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys	
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Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu	
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Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln	
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Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu	
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Glu	Gly	Asp	Thr	Ala	Leu	His	Val	Ala	Leu	Gln	Arg	His	Gln	Leu	Leu		
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ccc	ctg	gtg	gct	gat	ggg	gcc	ggg	ggg	gac	cca	ggg	ccc	ttg	cag	ctg	2417	
Pro	Leu	Val	Ala	Asp	Gly	Ala	Gly	Gly	Asp	Pro	Gly	Pro	Leu	Gln	Leu		
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ctg	tcc	agg	cta	cag	gcc	tcg	ggc	ctc	ccc	ggc	agc	gcg	gag	ctg	acg	2465	
Leu	Ser	Arg	Leu	Gln	Ala	Ser	Gly	Leu	Pro	Gly	Ser	Ala	Glu	Leu	Thr		
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Val	Gly	Ala	Ala	Val	Ala	Cys	Phe	Leu	Ala	Leu	Glu	Gly	Ala	Asp	Val		
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Ser	Tyr	Thr	Asn	His	Arg	Gly	Arg	Ser	Pro	Leu	Asp	Leu	Ala	Ala	Glu		
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ggt	cgc	gtg	ctc	aag	gcc	ctt	cag	ggc	tgc	gcc	cag	cgc	ttc	cgg	gag	2609	
Gly	Arg	Val	Leu	Lys	Ala	Leu	Gln	Gly	Cys	Ala	Gln	Arg	Phe	Arg	Glu		
	825					830					835						
cgg	cag	gcg	ggc	ggg	ggc	gcg	gcc	ccg	ggc	ccc	agg	caa	acg	ctc	ggg	2657	
Arg	Gln	Ala	Gly	Gly	Gly	Ala	Ala	Pro	Gly	Pro	Arg	Gln	Thr	Leu	Gly		
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acc	ccc	aac	acc	gtg	acg	aac	ctg	cac	gtg	ggc	gcc	gcg	ccg	ggg	ccc	2705	
Thr	Pro	Asn	Thr	Val	Thr	Asn	Leu	His	Val	Gly	Ala	Ala	Pro	Gly	Pro		
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gag	gcc	gct	gag	tgc	ctg	gtg	tgc	tcc	gag	ctg	gcg	ctg	ctg	gtg	ctg	2753	
Glu	Ala	Ala	Glu	Cys	Leu	Val	Cys	Ser	Glu	Leu	Ala	Leu	Leu	Val	Leu		
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ttc	tcg	ccg	tgc	cag	cac	cgc	acc	gtg	tgt	gag	gag	tgc	gcg	cgc	agg	2801	
Phe	Ser	Pro	Cys	Gln	His	Arg	Thr	Val	Cys	Glu	Glu	Cys	Ala	Arg	Arg		
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Met	Lys	Lys	Cys	Ile	Arg	Cys	Gln	Val	Val	Val	Ser	Lys	Lys	Leu	Arg		
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Pro	Asp	Gly	Ser	Glu	Val	Ala	Ser	Ala	Ala	Pro	Ala	Pro	Gly	Pro	Pro		
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Arg	Gln	Leu	Val	Glu	Glu	Leu	Gln	Ser	Arg	Tyr	Arg	Gln	Met	Glu	Glu		
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cgc	atc	acc	tgc	ccc	atc	tgc	atc	gac	agg	cac	atc	cgc	ctc	gtg	ttc	2993	
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955

960

965

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tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089
 Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
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Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
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Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
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Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
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Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
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Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
 115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
 130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
 145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
 165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
 180 185 190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
 195 200 205
 Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
 210 215 220
 Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
 225 230 235 240
 Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
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 Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
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 Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
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 Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
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 Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
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 Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
 325 330 335
 Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
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 Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
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 His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
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 Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
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 Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
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 Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
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 Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
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 Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
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Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val	545	550	555
Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser	565	570	575
Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg	580	585	590
Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser	595	600	605
Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly	610	615	620
Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr	625	630	635
Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His	645	650	655
Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp	660	665	670
Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn	675	680	685
Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp	690	695	700
Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val	705	710	715
Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys	725	730	735
Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala	740	745	750
Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly	755	760	765
Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu	770	775	780
Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu	785	790	795
			800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
805 810 815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
820 825 830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
835 840 845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
850 855 860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865 870 875 880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
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Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
900 905 910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
915 920 925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
930 935 940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945 950 955 960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
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Met Gly Trp Lys Pro Ser Glu
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gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161
Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
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agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga 209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
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gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
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Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
60 65 70

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Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
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Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
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acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
105 110 115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
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gac tgc tgc aag aag cac ggc ctg cgg ggc atg cgc tgg aag tgc cgt 545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
140 145 150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
155 160 165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
170 175 180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg 689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
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Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
220 225 230

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Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp	
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Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val	
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Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp	
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His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser	
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Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu	
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Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn	
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Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile	
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Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala	
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Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr	
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440	445 450 455
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Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys	

460

465

470

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Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala	
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Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu	
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Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln	
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Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu	
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Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu	
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Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr	
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Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val	
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Arg Gln Ala Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly	
840 845 850 855	
acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc	2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro	
860 865 870	
gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg	2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu	
875 880 885	
ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg	2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg	
890 895 900	
atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc	2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg	
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Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
940 945 950

cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc 2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe
955 960 965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
970 975 980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
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Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
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Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
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Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
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Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
100 105 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
130 135 140

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Gln	Cys	Tyr	Met	His	Asn	Lys	His	Glu	Leu	Ala	His	Ala	Phe	Asp	Arg	165	170	175	
Tyr	Glu	Thr	Ala	His	Ser	Arg	Pro	Val	Thr	Leu	Ser	Pro	Arg	Gln	Gly	180	185	190	
Leu	Pro	Arg	Ile	Pro	Leu	Arg	Gly	Ile	Phe	Gln	Gly	Ala	Lys	Val	Val	195	200	205	
Arg	Gly	Pro	Phe	Trp	Glu	Trp	Gly	Ser	Gln	Asp	Gly	Gly	Glu	Gly	Lys	210	215	220	
Pro	Gly	Arg	Val	Val	Asp	Ile	Arg	Gly	Trp	Asp	Val	Glu	Thr	Gly	Arg	225	230	235	240
Ser	Val	Ala	Ser	Val	Thr	Trp	Ala	Asp	Gly	Thr	Thr	Asn	Val	Tyr	Arg	245	250	255	
Val	Gly	His	Lys	Gly	Lys	Val	Asp	Leu	Lys	Cys	Val	Gly	Glu	Ala	Ala	260	265	270	
Gly	Gly	Phe	Tyr	Tyr	Lys	Asp	His	Leu	Pro	Arg	Leu	Gly	Lys	Pro	Ala	275	280	285	
Glu	Leu	Gln	Arg	Arg	Val	Ser	Ala	Asp	Ser	Gln	Pro	Phe	Gln	His	Gly	290	295	300	
Asp	Lys	Val	Lys	Cys	Leu	Leu	Asp	Thr	Asp	Val	Leu	Arg	Glu	Met	Gln	305	310	315	320
Glu	Gly	His	Gly	Gly	Trp	Asn	Pro	Arg	Met	Ala	Glu	Phe	Ile	Gly	Gln	325	330	335	
Thr	Gly	Thr	Val	His	Arg	Ile	Thr	Asp	Arg	Gly	Asp	Val	Arg	Val	Gln	340	345	350	
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His	His	Ser	Phe	Trp	Val	Gly	Asp	Val	Val	Arg	Val	Ile	Gly	Asp	Leu	370	375	380	
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Pro	Ser	Cys	Leu	Val	Ala	Tyr	Arg	Pro	Glu	Glu	Asp	Ala	Asn	Leu	Asp	435	440	445	

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 Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
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 Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
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Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
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 Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
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 Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
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Met Ile Ala Trp Arg Leu Pro Leu
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Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala
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Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr
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Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu
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Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu
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Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln
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Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
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Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr
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Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp
140 145 150

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Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala
155 160 165

gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg 642

Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser
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gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc 690

Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile
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Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro	
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Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu	
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Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu	
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Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu	
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Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys	
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Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp	
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Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala	
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Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp	
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Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu	
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Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile	
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Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala	
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Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu	
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Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu	
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Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe	
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Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu	
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Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp	
585 590 595 600	
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Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr	
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Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala	
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Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly	
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Ser	Thr	Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys		
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ctg	gac	ttc	ggg	atc	ttc	cgc	cgc	atc	ctc	cat	gtg	ctc	tac	aca	gac	2178	
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 Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly

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Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	Val	Ser	Phe	Gln	Val	Pro
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Leu	Ile	Leu	Arg	Gly	Leu	Tyr	Gln	Arg	Lys	Tyr	Leu	Tyr	Gln	Lys	Val
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Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln
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Phe	Phe	Tyr	Val	Asp	Val	Ser	Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr
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Gln	Leu	Arg	Val	Asn	Arg	Val	Asp	Asn	Phe	Val	Leu	Arg	Thr	Gly	Glu
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Leu	Phe	Thr	Phe	Asn	Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr
				165					170					175	
Glu	Phe	Pro	Asp	Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Lys
			180				185						190		
Lys	Ala	Phe	Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro
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Val	Tyr	Asp	Leu	Asp	Asn	Ser	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr
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Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	Cys
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Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Val	Glu	Asp	Glu	Pro	Val	Asp
			260					265					270		
Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	Gln	Ala	Val
		275					280					285			
Thr	Ser	Glu	Ala	Tyr	Val	Gly	Gly	Met	Leu	Phe	Cys	Leu	Gly	Ile	Phe
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Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	Cys	Trp	Glu	Asn	Trp
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Arg	Gln	Arg	Lys	Lys	Thr	Leu	Leu	Val	Ala	Ile	Asp	Arg	Ala	Cys	Pro
			325					330					335		
Glu	Ser	Gly	His	Ala	Arg	Val	Leu	Ala	Asp	Ser	Phe	Pro	Gly	Ser	Ala
			340				345					350			
Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly	Ser	Phe	Glu	Asn	Gly	Ser	Gly	Ser

355	360	365
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Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe 465 470 475 480		
Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val 485 490 495		
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His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu 515 520 525		
Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg 530 535 540		
Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu 545 550 555 560		
Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr 565 570 575		
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro 580 585 590		
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Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn 610 615 620		
Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe 625 630 635 640		
Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile 645 650 655		
Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln		

660

665

670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg
675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
690 695 700

Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
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Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp
835 840 845

Lys Ile Tyr Val Phe
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Met Phe Ala Leu Gly Leu Pro Phe Leu Val
1 5 10

ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag 161

Leu	Leu	Val	Ala	Ser	Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	
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Asn	Val	Ser	Gln	Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	
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gtc	aac	agc	gag	ctg	gtc	aac	atc	tac	acc	ttc	aac	cat	act	gtg	acc	257
Val	Asn	Ser	Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	
		45					50					55				
cgc	aac	agg	aca	gag	ggc	gtg	cgt	gtg	tct	gtg	aac	gtc	ctg	aac	aag	305
Arg	Asn	Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	
	60					65					70					
cag	aag	ggg	gcg	ccg	ttg	ctg	ttt	gtg	gtc	cgc	cag	aag	gag	gct	gtg	353
Gln	Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	
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gtg	tcc	ttc	cag	gtg	ccc	cta	atc	ctg	cga	ggg	atg	ttt	cag	cgc	aag	401
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	Lys	
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tac	ctc	tac	caa	aaa	gtg	gaa	cga	acc	ctg	tgt	cag	ccc	ccc	acc	aag	449
Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	Thr	Lys	
			110					115				120				
aat	gag	tcg	gag	att	cag	ttc	ttc	tac	gtg	gat	gtg	tcc	acc	ctg	tca	497
Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	Thr	Leu	Ser	
		125					130					135				
cca	gtc	aac	acc	aca	tac	cag	ctc	cgg	gtc	agc	cgc	atg	gac	gat	ttt	545
Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	Met	Asp	Asp	Phe	
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gtg	ctc	agg	act	ggg	gag	cag	ttc	agc	ttc	aat	acc	aca	gca	gca	cag	593
Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	Thr	Thr	Ala	Ala	Gln	
	155				160					165					170	
ccc	cag	tac	ttc	aag	tat	gag	ttc	cct	gaa	ggc	gtg	gac	tcg	gta	att	641
Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	Gly	Val	Asp	Ser	Val	Ile	
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gtc	aag	gtg	acc	tcc	aac	aag	gcc	ttc	ccc	tgc	tca	gtc	atc	tcc	att	689
Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	Pro	Cys	Ser	Val	Ile	Ser	Ile	
			190				195						200			
cag	gat	gtg	ctg	tgt	cct	gtc	tat	gac	ctg	gac	aac	aac	gta	gcc	ttc	737
Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	
		205					210					215				
atc	ggc	atg	tac	cag	acg	atg	acc	aag	aag	gcg	gcc	atc	acc	gta	cag	785
Ile	Gly	Met	Tyr	Gln	Thr	Met	Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	
	220					225					230					
cgc	aaa	gac	ttc	ccc	agc	aac	agc	ttt	tat	gtg	gtg	gtg	gtg	gtg	aag	833
Arg	Lys	Asp	Phe	Pro	Ser	Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	

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Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala	255	260	265	
gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg				929
Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val	270	275	280	
ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc				977
Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu	285	290	295	
ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg				1025
Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu	300	305	310	
gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc				1073
Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala	315	320	325	330
att gac cga gcc tgc cca gaa agc ggt cac cct cga gtc ctg gct gat				1121
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp	335	340	345	
tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt				1169
Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe	350	355	360	
gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act				1217
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr	365	370	375	
ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc				1265
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg	380	385	390	
ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc				1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser	395	400	405	410
ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg				1361
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	415	420	425	
gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat				1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn	430	435	440	
gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag				1457
Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys	445	450	455	
gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att				1505
Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile	460	465	470	

gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc	1553
Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile	
475 480 485 490	
acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac	1601
Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr	
495 500 505	
tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac	1649
Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn	
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aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg	1697
Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu	
525 530 535	
ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc	1745
Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg	
540 545 550	
aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt	1793
Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu	
555 560 565 570	
ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct	1841
Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala	
575 580 585	
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Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser	
590 595 600	
ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag	1937
Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys	
605 610 615	
cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg	1985
Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu	
620 625 630	
gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg	2033
Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly	
635 640 645 650	
aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc	2081
Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr	
655 660 665	
ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac	2129
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp	
670 675 680	
tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc	2177
Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile	
685 690 695	

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc	2225
Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val	
700 705 710	
atg ggc aac gtc atc aac tgg tgc ctg gct gcc tat ggg ctt atc atg	2273
Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met	
715 720 725 730	
cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac	2321
Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn	
735 740 745	
ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg	2369
Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly	
750 755 760	
gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg	2417
Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val	
765 770 775	
gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg	2465
Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp	
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cag aaa acc cct gca gag tgc agg gag cac aac cgg gac tgc atc ctc	2513
Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu	
795 800 805 810	
ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc	2561
Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile	
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gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg	2609
Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly	
830 835 840	
tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg	2658
Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly	
845 850 855	
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Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	Glu	Leu	Val
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	65					70				75					80
Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	Val	Ser	Phe	Gln	Val	Pro
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Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	Lys	Tyr	Leu	Tyr	Gln	Lys	Val
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				165					170					175	
Glu	Phe	Pro	Glu	Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn
			180					185					190		
Lys	Ala	Phe	Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro
		195					200					205			
Val	Tyr	Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr
	210					215					220				
Met	Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser
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Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	Cys
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Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	Val	Asp
			260					265					270		

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
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 Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
 290 295 300
 Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
 305 310 315 320
 Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
 325 330 335
 Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser
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 Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser
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 Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly
 370 375 380
 Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
 385 390 395 400
 Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
 405 410 415
 Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
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 Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
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 Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
 450 455 460
 Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
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 Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
 485 490 495
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 His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
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 Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
 530 535 540
 Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu
 545 550 555 560
 Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
 565 570 575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
 580 585 590
 Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
 595 600 605
 Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
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 Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
 625 630 635 640
 Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
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 Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg
 675 680 685
 Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
 690 695 700
 Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn
 705 710 715 720
 Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
 725 730 735
 Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
 740 745 750
 Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
 755 760 765
 Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
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 Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
 785 790 795 800
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 805 810 815
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
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Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu
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gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat 154
Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr
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cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg 202
Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg
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tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc 250
Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe
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ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile
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cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn
                    85                      90                      95

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag 394
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
                    100                      105                      110

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct 442
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
                    115                      120                      125

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc 490
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
                    130                      135                      140                      145

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct 538
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro
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ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
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 cagagtaaac ttgaagcaga tctgtgcatg cttttcctct gcaacaattg gctcgtttct 2751
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<210> 168

<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

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Tyr	Pro	Thr	Tyr	Tyr	Ile	Cys	Arg	Ser	Tyr	Glu	Asp	Cys	Cys	Gly	Ser	35	40	45	
Arg	Cys	Cys	Val	Arg	Ala	Leu	Ser	Ile	Gln	Arg	Leu	Trp	Tyr	Phe	Trp	50	55	60	
Phe	Leu	Leu	Met	Met	Gly	Val	Leu	Phe	Cys	Cys	Gly	Ala	Gly	Phe	Phe	65	70	75	80
Ile	Arg	Arg	Arg	Met	Tyr	Pro	Pro	Pro	Leu	Ile	Glu	Glu	Pro	Ala	Phe	85	90	95	
Asn	Val	Ser	Tyr	Thr	Arg	Gln	Pro	Pro	Asn	Pro	Gly	Pro	Gly	Ala	Gln	100	105	110	
Gln	Pro	Gly	Pro	Pro	Tyr	Tyr	Thr	Asp	Pro	Gly	Gly	Pro	Gly	Met	Asn	115	120	125	
Pro	Val	Gly	Asn	Ser	Met	Ala	Met	Ala	Phe	Gln	Val	Pro	Pro	Asn	Ser	130	135	140	
Pro	Gln	Gly	Ser	Val	Ala	Cys	Pro	Pro	Pro	Pro	Ala	Tyr	Cys	Asn	Thr	145	150	155	160
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<210> 169
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (136)..(1755)

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 agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171
 Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile
 1 5 10
 tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219
 Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu
 15 20 25
 cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267
 Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala
 30 35 40
 acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315
 Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn
 45 50 55 60
 acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363
 Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu
 65 70 75
 agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411
 Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr
 80 85 90
 cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459
 Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu
 95 100 105
 cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507
 Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala
 110 115 120
 gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555
 Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr
 125 130 135 140
 ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603
 Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn
 145 150 155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat	651
Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn	
160 165 170	
cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc	699
Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser	
175 180 185	
cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt	747
Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser	
190 195 200	
acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct	795
Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro	
205 210 215 220	
gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg	843
Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg	
225 230 235	
gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc	891
Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr	
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Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu	
255 260 265	
ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc	987
Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser	
270 275 280	
agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc	1035
Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr	
285 290 295 300	
acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca	1083
Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro	
305 310 315	
gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc	1131
Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro	
320 325 330	
cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa	1179
Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys	
335 340 345	
ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct	1227
Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro	
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act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac	1275
Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp	
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ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta 1419
 Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val
 415 420 425

gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc 1467
 Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser
 430 435 440

acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat 1515
 Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr
 445 450 455 460

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563
 Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile
 465 470 475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611
 Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly
 480 485 490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659
 Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys
 495 500 505

cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg 1707
 His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly
 510 515 520

gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac 1755
 Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
 525 530 535 540

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<210> 170

<211> 540

<212> PRT

<213> Homo sapiens

<400> 170

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 20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
 35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
 50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu

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Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln						
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Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu						
	100		105		110	
Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile						
	115		120		125	
Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val						
	130		135		140	
Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala						
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Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly						
	165		170		175	
Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser						
	180		185		190	
Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala						
	195		200		205	
Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser						
	210		215		220	
Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu						
	225		230		235	240
Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser						
	245		250		255	
Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly						
	260		265		270	
Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu						
	275		280		285	
Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro						
	290		295		300	
Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser						
	305		310		315	320
Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val						
	325		330		335	
Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn						
	340		345		350	
Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val						
	355		360		365	
Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg						

370

375

380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385 390 395 400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
405 410 415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
435 440 445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
450 455 460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465 470 475 480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
485 490 495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
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Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
515 520 525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
530 535 540

<210> 171
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<212> DNA
<213> Homo sapiens

<220>
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<222> (242)..(3094)

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gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccc 180
gggaaggagg cagggcaagg ccgggcttgg gggcaggtgg tccgggcatc cagccttgaa 240
g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289
Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
1 5 10 15
gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337

Ala	Ala	Arg	Gln	Leu	Gly	Leu	Leu	Val	Asp	Leu	Ser	Pro	Asp	Gly	Leu		
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atg	atc	cct	gag	gac	ggg	gct	aac	gat	gaa	gaa	ctg	gag	gct	gag	ttc	385	
Met	Ile	Pro	Glu	Asp	Gly	Ala	Asn	Asp	Glu	Glu	Leu	Glu	Ala	Glu	Phe		
		35					40					45					
ttg	gct	ttg	gtc	ggg	ggc	cag	ccc	cca	gcc	ctg	gag	aag	ctc	aaa	ggc	433	
Leu	Ala	Leu	Val	Gly	Gly	Gln	Pro	Pro	Ala	Leu	Glu	Lys	Leu	Lys	Gly		
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aaa	ggt	ccc	ttg	ccg	atg	gag	gcc	att	gag	aag	atg	gcc	agc	ctg	tgc	481	
Lys	Gly	Pro	Leu	Pro	Met	Glu	Ala	Ile	Glu	Lys	Met	Ala	Ser	Leu	Cys		
	65				70				75						80		
atg	aga	gac	ccg	gat	gag	gat	gag	gag	gag	ggg	acg	gat	gag	gac	gac	529	
Met	Arg	Asp	Pro	Asp	Glu	Asp	Glu	Glu	Glu	Gly	Thr	Asp	Glu	Asp	Asp		
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ttg	gag	gct	gat	gat	gac	ctg	ctg	gcg	gag	cta	aat	gag	gtc	ctt	gga	577	
Leu	Glu	Ala	Asp	Asp	Asp	Leu	Leu	Ala	Glu	Leu	Asn	Glu	Val	Leu	Gly		
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gag	gag	cag	aag	gct	tca	gag	acc	cca	cct	cct	gtg	gcc	cag	ccg	aag	625	
Glu	Glu	Gln	Lys	Ala	Ser	Glu	Thr	Pro	Pro	Pro	Val	Ala	Gln	Pro	Lys		
		115					120					125					
cct	gag	gcc	cct	cat	ccg	ggg	ctg	gag	acc	acc	ttg	cag	gag	agg	ctg	673	
Pro	Glu	Ala	Pro	His	Pro	Gly	Leu	Glu	Thr	Thr	Leu	Gln	Glu	Arg	Leu		
	130					135					140						
gcg	ctc	tat	cag	aca	gca	att	gaa	agc	gcc	aga	caa	gct	gga	gac	agc	721	
Ala	Leu	Tyr	Gln	Thr	Ala	Ile	Glu	Ser	Ala	Arg	Gln	Ala	Gly	Asp	Ser		
	145				150				155						160		
gcc	aag	atg	cgg	cgc	tac	gat	cgg	ggg	ctt	aaa	aca	ctg	gaa	aac	ctg	769	
Ala	Lys	Met	Arg	Arg	Tyr	Asp	Arg	Gly	Leu	Lys	Thr	Leu	Glu	Asn	Leu		
				165				170						175			
ctc	gcc	tcc	atc	cgt	aag	ggc	aat	gcc	att	gac	gaa	gcg	gac	atc	ccg	817	
Leu	Ala	Ser	Ile	Arg	Lys	Gly	Asn	Ala	Ile	Asp	Glu	Ala	Asp	Ile	Pro		
			180					185					190				
ccg	cca	gtg	gcc	ata	gga	aaa	ggc	ccg	gcg	tcc	acg	cct	acc	tac	agc	865	
Pro	Pro	Val	Ala	Ile	Gly	Lys	Gly	Pro	Ala	Ser	Thr	Pro	Thr	Tyr	Ser		
		195					200					205					
cct	gca	ccc	acc	cag	ccg	gcc	cct	aga	atc	gcg	tca	gcc	cca	gag	ccc	913	
Pro	Ala	Pro	Thr	Gln	Pro	Ala	Pro	Arg	Ile	Ala	Ser	Ala	Pro	Glu	Pro		
	210					215					220						
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Arg	Val	Thr	Leu	Glu	Gly	Pro	Ser	Ala	Thr	Ala	Pro	Ala	Ser	Ser	Pro		
	225				230				235						240		
ggc	ttg	gct	aag	ccc	cag	atg	ccc	cca	ggt	ccc	tgc	agc	cct	ggc	cct	1009	
Gly	Leu	Ala	Lys	Pro	Gln	Met	Pro	Pro	Gly	Pro	Cys	Ser	Pro	Gly	Pro		

245										250										255										
ctg	gcc	cag	ttg	cag	agc	cgc	cag	cgc	gac	tac	aag	ctg	gct	gcc	ctc	1057														
Leu	Ala	Gln	Leu	Gln	Ser	Arg	Gln	Arg	Asp	Tyr	Lys	Leu	Ala	Ala	Leu															
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cac	gcc	aag	cag	cag	gga	gat	acc	act	gct	gcc	gct	aga	cac	ttc	cgc	1105														
His	Ala	Lys	Gln	Gln	Gly	Asp	Thr	Thr	Ala	Ala	Ala	Arg	His	Phe	Arg															
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gtg	gct	aag	agc	ttt	gat	gct	gtc	ttg	gag	gcc	ctg	agc	cgg	ggt	gag	1153														
Val	Ala	Lys	Ser	Phe	Asp	Ala	Val	Leu	Glu	Ala	Leu	Ser	Arg	Gly	Glu															
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ccc	gtg	gac	ctc	tcc	tgc	ctg	ccc	cct	cca	ccc	gac	cag	ctg	ccc	cca	1201														
Pro	Val	Asp	Leu	Ser	Cys	Leu	Pro	Pro	Pro	Pro	Asp	Gln	Leu	Pro	Pro															
			305							310							315													
gac	cca	ccg	tca	cca	ccg	tcg	cag	cct	ccg	acc	ccc	gct	acg	gcg	ccc	1249														
Asp	Pro	Pro	Ser	Pro	Pro	Ser	Gln	Pro	Pro	Thr	Pro	Ala	Thr	Ala	Pro															
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tcc	aca	aca	gag	gtg	ccc	cca	ccc	ccg	agg	acc	ctg	ctg	gag	gcg	ctg	1297														
Ser	Thr	Thr	Glu	Val	Pro	Pro	Pro	Pro	Arg	Thr	Leu	Leu	Glu	Ala	Leu															
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gag	cag	cgg	atg	gag	cgg	tac	cag	gtg	gcc	gca	gcc	cag	gcc	aag	agc	1345														
Glu	Gln	Arg	Met	Glu	Arg	Tyr	Gln	Val	Ala	Ala	Ala	Gln	Ala	Lys	Ser															
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aag	ggg	gac	cag	cgg	aaa	gct	cga	atg	cac	gag	cgc	atc	gtc	aag	caa	1393														
Lys	Gly	Asp	Gln	Arg	Lys	Ala	Arg	Met	His	Glu	Arg	Ile	Val	Lys	Gln															
			370							375							380													
tac	caa	gat	gcc	atc	cga	gcc	cac	aag	gct	ggc	cga	gcc	gtg	gat	gtc	1441														
Tyr	Gln	Asp	Ala	Ile	Arg	Ala	His	Lys	Ala	Gly	Arg	Ala	Val	Asp	Val															
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gct	gaa	ttg	ccc	gtg	ccc	cca	ggc	ttc	ccc	cca	atc	cag	ggc	ctg	gag	1489														
Ala	Glu	Leu	Pro	Val	Pro	Pro	Gly	Phe	Pro	Pro	Ile	Gln	Gly	Leu	Glu															
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gcc	acc	aag	ccc	acc	cag	cag	agt	ctg	gtg	ggt	gtc	ctg	gag	act	gcc	1537														
Ala	Thr	Lys	Pro	Thr	Gln	Gln	Ser	Leu	Val	Gly	Val	Leu	Glu	Thr	Ala															
			420							425							430													
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Met	Lys	Leu	Ala	Asn	Gln	Asp	Glu	Gly	Pro	Glu	Asp	Glu	Glu	Asp	Glu															
			435							440							445													
gtg	cct	aag	aag	cag	aac	agc	cct	gtg	gcc	ccc	aca	gcc	cag	ccc	aaa	1633														
Val	Pro	Lys	Lys	Gln	Asn	Ser	Pro	Val	Ala	Pro	Thr	Ala	Gln	Pro	Lys															
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gcc	cca	ccc	tca	aga	act	ccc	cag	tcg	gga	tca	gcc	cca	aca	gcc	aaa	1681														
Ala	Pro	Pro	Ser	Arg	Thr	Pro	Gln	Ser	Gly	Ser	Ala	Pro	Thr	Ala	Lys															
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																		480												

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc	1729
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe	
485 490 495	
cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag	1777
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys	
500 505 510	
cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag	1825
Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys	
515 520 525	
gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac	1873
Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp	
530 535 540	
atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg	1921
Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu	
545 550 555 560	
gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat	1969
Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr	
565 570 575	
ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac	2017
Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn	
580 585 590	
cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag	2065
His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys	
595 600 605	
ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag	2113
Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys	
610 615 620	
caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa	2161
Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln	
625 630 635 640	
agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac	2209
Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp	
645 650 655	
atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga	2257
Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly	
660 665 670	
ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat	2305
Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr	
675 680 685	
ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac	2353
Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn	
690 695 700	

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc	2401
Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg	
705 710 715 720	
agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc	2449
Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe	
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gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg	2497
Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly	
740 745 750	
aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg	2545
Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg	
755 760 765	
gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg	2593
Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu	
770 775 780	
gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag	2641
Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu	
785 790 795 800	
acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg	2689
Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val	
805 810 815	
ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc	2737
Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala	
820 825 830	
cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc	2785
Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu	
835 840 845	
agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc	2833
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala	
850 855 860	
ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac	2881
Leu Arg Gln Ala Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr	
865 870 875 880	
cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag	2929
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln	
885 890 895	
ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag	2977
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln	
900 905 910	
ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc	3025
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser	
915 920 925	
agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt	3073

Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
 930 935 940

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 Glu Leu Gln Arg Leu Arg Arg
 945 950

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<211> 951

<212> PRT

<213> Homo sapiens

<400> 172

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Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
 35 40 45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
 50 55 60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
 65 70 75 80

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
 85 90 95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
 100 105 110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
 115 120 125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
 130 135 140

Ala	Leu	Tyr	Gln	Thr	Ala	Ile	Glu	Ser	Ala	Arg	Gln	Ala	Gly	Asp	Ser	145	150	155	160
Ala	Lys	Met	Arg	Arg	Tyr	Asp	Arg	Gly	Leu	Lys	Thr	Leu	Glu	Asn	Leu	165	170	175	
Leu	Ala	Ser	Ile	Arg	Lys	Gly	Asn	Ala	Ile	Asp	Glu	Ala	Asp	Ile	Pro	180	185	190	
Pro	Pro	Val	Ala	Ile	Gly	Lys	Gly	Pro	Ala	Ser	Thr	Pro	Thr	Tyr	Ser	195	200	205	
Pro	Ala	Pro	Thr	Gln	Pro	Ala	Pro	Arg	Ile	Ala	Ser	Ala	Pro	Glu	Pro	210	215	220	
Arg	Val	Thr	Leu	Glu	Gly	Pro	Ser	Ala	Thr	Ala	Pro	Ala	Ser	Ser	Pro	225	230	235	240
Gly	Leu	Ala	Lys	Pro	Gln	Met	Pro	Pro	Gly	Pro	Cys	Ser	Pro	Gly	Pro	245	250	255	
Leu	Ala	Gln	Leu	Gln	Ser	Arg	Gln	Arg	Asp	Tyr	Lys	Leu	Ala	Ala	Leu	260	265	270	
His	Ala	Lys	Gln	Gln	Gly	Asp	Thr	Thr	Ala	Ala	Ala	Arg	His	Phe	Arg	275	280	285	
Val	Ala	Lys	Ser	Phe	Asp	Ala	Val	Leu	Glu	Ala	Leu	Ser	Arg	Gly	Glu	290	295	300	
Pro	Val	Asp	Leu	Ser	Cys	Leu	Pro	Pro	Pro	Pro	Asp	Gln	Leu	Pro	Pro	305	310	315	320
Asp	Pro	Pro	Ser	Pro	Pro	Ser	Gln	Pro	Pro	Thr	Pro	Ala	Thr	Ala	Pro	325	330	335	
Ser	Thr	Thr	Glu	Val	Pro	Pro	Pro	Pro	Arg	Thr	Leu	Leu	Glu	Ala	Leu	340	345	350	
Glu	Gln	Arg	Met	Glu	Arg	Tyr	Gln	Val	Ala	Ala	Ala	Gln	Ala	Lys	Ser	355	360	365	
Lys	Gly	Asp	Gln	Arg	Lys	Ala	Arg	Met	His	Glu	Arg	Ile	Val	Lys	Gln	370	375	380	
Tyr	Gln	Asp	Ala	Ile	Arg	Ala	His	Lys	Ala	Gly	Arg	Ala	Val	Asp	Val	385	390	395	400
Ala	Glu	Leu	Pro	Val	Pro	Pro	Gly	Phe	Pro	Pro	Ile	Gln	Gly	Leu	Glu	405	410	415	
Ala	Thr	Lys	Pro	Thr	Gln	Gln	Ser	Leu	Val	Gly	Val	Leu	Glu	Thr	Ala	420	425	430	
Met	Lys	Leu	Ala	Asn	Gln	Asp	Glu	Gly	Pro	Glu	Asp	Glu	Glu	Asp	Glu	435	440	445	

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
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 Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
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 Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
 485 490 495
 Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
 500 505 510
 Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
 515 520 525
 Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
 530 535 540
 Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
 545 550 555 560
 Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
 565 570 575
 Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
 580 585 590
 His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
 595 600 605
 Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
 610 615 620
 Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
 625 630 635 640
 Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
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 Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
 660 665 670
 Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
 675 680 685
 Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
 690 695 700
 Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
 705 710 715 720
 Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
 725 730 735
 Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
 740 745 750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
 755 760 765
 Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
 770 775 780
 Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
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 Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
 820 825 830
 Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
 835 840 845
 Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
 850 855 860
 Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
 865 870 875 880
 Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
 885 890 895
 Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
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 Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
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 Glu Leu Gln Arg Leu Arg Arg
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<211> 2796

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (574)..(1683)

<400> 173

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			Met	Gly	Asp	Arg	Arg		Phe	Ile						
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gac	ttc	caa	ttc	caa	gat	tta	aat	tca	agt	ctc	aga	ccc	agg	ttg	gga	642
Asp	Phe	Gln	Phe	Gln	Asp	Leu	Asn	Ser	Ser	Leu	Arg	Pro	Arg	Leu	Gly	
		10					15					20				
aat	gca	act	gcc	aat	aat	act	tgc	att	gtt	gat	gat	tcc	ttc	aag	tat	690
Asn	Ala	Thr	Ala	Asn	Asn	Thr	Cys	Ile	Val	Asp	Asp	Ser	Phe	Lys	Tyr	
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aat	ttg	aat	ggg	gct	gtc	tat	agt	gtt	gta	ttc	atc	ctg	ggg	cta	ata	738
Asn	Leu	Asn	Gly	Ala	Val	Tyr	Ser	Val	Val	Phe	Ile	Leu	Gly	Leu	Ile	
	40				45					50					55	
acc	aac	agt	gcc	tcc	ctg	ttt	gtc	ttc	tgc	ttc	cgc	atg	aaa	atg	aga	786
Thr	Asn	Ser	Ala	Ser	Leu	Phe	Val	Phe	Cys	Phe	Arg	Met	Lys	Met	Arg	
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agt	gag	acg	gct	act	ttc	atc	acc	aac	ctg	gcc	ctc	tct	gat	ttg	ctt	834
Ser	Glu	Thr	Ala	Thr	Phe	Ile	Thr	Asn	Leu	Ala	Leu	Ser	Asp	Leu	Leu	
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ttt	gtt	tgt	acc	cta	cct	ttc	aaa	ata	ttt	tac	aac	ttt	aat	cgc	cac	882
Phe	Val	Cys	Thr	Leu	Pro	Phe	Lys	Ile	Phe	Tyr	Asn	Phe	Asn	Arg	His	
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tgg	cct	ttt	ggg	gac	acc	ctc	tgt	aag	atc	tca	ggg	act	gcg	ttc	ctc	930
Trp	Pro	Phe	Gly	Asp	Thr	Leu	Cys	Lys	Ile	Ser	Gly	Thr	Ala	Phe	Leu	
	105					110					115					
acc	aac	atc	tat	ggg	agc	atg	ctc	ttc	ctc	acc	tgc	atc	agt	gtg	gat	978
Thr	Asn	Ile	Tyr	Gly	Ser	Met	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Val	Asp	
	120				125					130				135		
cgt	ttc	cta	gcc	att	gtc	tat	ccc	ttc	cga	tgc	cgt	acc	atc	agg	acc	1026
Arg	Phe	Leu	Ala	Ile	Val	Tyr	Pro	Phe	Arg	Ser	Arg	Thr	Ile	Arg	Thr	
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agg	agg	aat	tcc	gcc	att	gtg	tgc	gct	gga	gtc	tgg	atc	cta	gtc	ctc	1074
Arg	Arg	Asn	Ser	Ala	Ile	Val	Cys	Ala	Gly	Val	Trp	Ile	Leu	Val	Leu	
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agt	ggg	ggg	att	tca	gct	tct	ttg	ttc	tcc	acc	act	aat	gtc	aac	aat	1122

Ser	Gly	Gly	Ile	Ser	Ala	Ser	Leu	Phe	Ser	Thr	Thr	Asn	Val	Asn	Asn		
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Ala	Thr	Thr	Thr	Cys	Phe	Glu	Gly	Phe	Ser	Lys	Arg	Val	Trp	Lys	Thr		
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Tyr	Leu	Ser	Lys	Ile	Thr	Ile	Phe	Ile	Glu	Val	Val	Gly	Phe	Ile	Ile		
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cct	ctg	ata	ttg	aat	gtt	tct	tgt	tct	tct	gtg	gtg	ctt	aga	acc	ctc	1266	
Pro	Leu	Ile	Leu	Asn	Val	Ser	Cys	Ser	Ser	Val	Val	Leu	Arg	Thr	Leu		
				220					225					230			
cgc	aag	cct	gca	aca	ttg	tct	cag	att	ggg	acc	aat	aag	aaa	aaa	gtg	1314	
Arg	Lys	Pro	Ala	Thr	Leu	Ser	Gln	Ile	Gly	Thr	Asn	Lys	Lys	Lys	Val		
			235					240					245				
ttg	aag	atg	atc	aca	gtg	cat	atg	gca	gtg	ttt	gtg	gta	tgc	ttt	gta	1362	
Leu	Lys	Met	Ile	Thr	Val	His	Met	Ala	Val	Phe	Val	Val	Cys	Phe	Val		
		250					255					260					
cca	tac	aac	tcc	gtt	ctc	ttt	tta	tat	gcc	ttg	gta	cgc	tcc	caa	gcc	1410	
Pro	Tyr	Asn	Ser	Val	Leu	Phe	Leu	Tyr	Ala	Leu	Val	Arg	Ser	Gln	Ala		
	265					270					275						
att	act	aat	tgc	tta	ttg	gaa	agg	ttt	gca	aag	atc	atg	tac	cca	att	1458	
Ile	Thr	Asn	Cys	Leu	Leu	Glu	Arg	Phe	Ala	Lys	Ile	Met	Tyr	Pro	Ile		
280					285					290					295		
acc	ttg	tgc	ctt	gca	act	ctg	aat	tgt	tgc	ttt	gat	cct	ttt	atc	tat	1506	
Thr	Leu	Cys	Leu	Ala	Thr	Leu	Asn	Cys	Cys	Phe	Asp	Pro	Phe	Ile	Tyr		
				300					305					310			
tac	ttc	act	ctt	gaa	tcc	ttt	cag	aag	tcc	ttt	tat	atc	aat	aca	cat	1554	
Tyr	Phe	Thr	Leu	Glu	Ser	Phe	Gln	Lys	Ser	Phe	Tyr	Ile	Asn	Thr	His		
			315					320					325				
ata	agg	atg	gag	tcg	ctg	ttt	aag	act	gag	aca	cct	ctg	acc	ccc	aaa	1602	
Ile	Arg	Met	Glu	Ser	Leu	Phe	Lys	Thr	Glu	Thr	Pro	Leu	Thr	Pro	Lys		
		330					335					340					
cct	tcc	ctt	cca	gct	atc	caa	gag	gaa	gtt	agt	gat	caa	aca	aca	aat	1650	
Pro	Ser	Leu	Pro	Ala	Ile	Gln	Glu	Glu	Val	Ser	Asp	Gln	Thr	Thr	Asn		
		345				350					355						
aat	ggt	ggt	gaa	tta	atg	ctg	gaa	tcc	acc	ttc	taggtaccag	aattgtcttt				1703	
Asn	Gly	Gly	Glu	Leu	Met	Leu	Glu	Ser	Thr	Phe							
360					365					370							
caggttcagc	tacagtgtct	cttatgattt	ttttcctatg	ctataaatag	gagaaacaaa											1763	
ttgaagctaa	tgatactgag	aatagagtaa	tgtaccaa	at	gcagtcagat	acatttgttt										1823	
gaacactatt	gtacatat	ttc	tgttttgttc	agtaattata	ggccaagtct	aattacaaca										1883	

accaaaacag atcagcctct tctgttgagt tgacttttca ttacctaaat gaccagtggg 1943
 cttgactttt agtgatgtga gggttatttt taaacttaaa aaaaaaggca ttccagtaat 2003
 tttggtaatt ggggtgggcc tataaatata gaacaaattc agggattatt taaaaacatc 2063
 tgtgttacta ctgatatatg ctagtatttt tttccttttt tgaattaata ttgaatttat 2123
 tttaaaaaaa gaactatttt tacctaattc taataagaca tactgagaaa gagaaatgtg 2183
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 attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363
 gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423
 ttaacagtgt caatttaaaa aaaaaaaaaac ttaagcaac actataattt ttcttaagat 2483
 tttcatttat cctttatggg ggtggggatt ggcttgtaga aaatatttat tcttcatgtt 2543
 aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccagg tcaggagtaa 2603
 attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663
 tttttaaggt ggtgggttaga tagctgtaat tttgaaatcc atactctctt ctgtacattt 2723
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 aagatgtgta cat 2796

<210> 174
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 174
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 Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
 20 25 30
 Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
 35 40 45
 Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe
 50 55 60
 Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn
 65 70 75 80
 Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
 85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
 100 105 110
 Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
 115 120 125
 Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
 130 135 140
 Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
 145 150 155 160
 Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
 165 170 175
 Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
 180 185 190
 Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
 195 200 205
 Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
 210 215 220
 Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
 225 230 235 240
 Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
 245 250 255
 Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
 260 265 270
 Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe
 275 280 285
 Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
 290 295 300
 Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
 305 310 315 320
 Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
 325 330 335
 Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
 340 345 350
 Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
 355 360 365
 Thr Phe
 370

<210> 175

<211> 2299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (67)..(1176)

<400> 175
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aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca 108
 Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser
 1 5 10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156
 Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr
 15 20 25 30

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204
 Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr
 35 40 45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252
 Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe
 50 55 60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300
 Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
 65 70 75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348
 Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
 80 85 90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc 396
 Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu
 95 100 105 110

tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg 444
 Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met
 115 120 125

ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat 492
 Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr
 130 135 140

cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg 540
 Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val
 145 150 155

tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct 588
 Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser
 160 165 170

ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa 636
 Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu

175	180	185	190	
ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata				684
Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile				
195	200	205		
ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct				732
Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser				
210	215	220		
tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct				780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser				
225	230	235		
caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat				828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His				
240	245	250		
atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc				876
Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe				
255	260	265		270
ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa				924
Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu				
275	280	285		
aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg				972
Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu				
290	295	300		
aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt				1020
Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe				
305	310	315		
cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt				1068
Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe				
320	325	330		
aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa				1116
Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln				
335	340	345	350	
gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta				1164
Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu				
355	360	365		
gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc				1216
Glu Ser Thr Phe				
370				
ctataatttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc				1276
accaaatacca gtcagataca tttgtttgaa ggtatactgt agagttttta ttgctgtttt				1336
gttcagtaat tatagggtcaa atctaattac aacaaccaag atggattgcc aaactcttct				1396
gcttggttgg aatttcattg tatogcatta tccaggtggc tagtggcatt tgataatata				1456

gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516
tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576
atgctagttt tattttattt ttttgactg tcattgagtt tatttttagca caagaatatt 1636
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tgtgcatttt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756
aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcgtt 1816
gtttttacac caaattaaaa tttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876
gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936
tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996
gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056
ctgcatttgt gcccaggtca ggagcaaatt gaaaaaaaa ataaagtaat actaaaaaat 2116
caaactataa acccaaaaca tttattaaaa cctgaattaa tcctttttgg agggaggagt 2176
agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236
caggagctgc tgaatttgtg cccctggatt ggaaccaaat aaaaaaaaa aaaaaaatt 2296
cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser
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Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe
50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
65 70 75 80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys

100

105

110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
 115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
 130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
 145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
 165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
 180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
 195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
 210 215 220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
 225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
 245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
 260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
 275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
 290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
 305 310 315 320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
 325 330 335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
 340 345 350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
 355 360 365

Thr Phe
 370

<210> 177

<211> 973

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (30)..(416)

<400> 177

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ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 101
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
   10                               15                               20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
   25                               30                               35                               40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
                   45                               50                               55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
                   60                               65                               70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
                   75                               80                               85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341
Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
   90                               95                               100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
  105                               110                               115                               120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgccca 436
Gly Cys Pro Ala Val Ala Leu Ile Gln
                   125

gccggggctc gccactcat cattcattca tccattctag agccagtctc tgccctccag 496

acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgccctctggc 616

tccagaacag aaaggagacc tcacgtggc tcacacaaaa cagctgacac tgactaagga 676

actgcagcat ttgcacaggg gaggggggtg cctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggc ccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggccacta 856
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ggagggctgg ccctaagata cagaccccc caactcccc aagcggggag gagatattta 916
 ttttggggag agtttggagg ggagggagaa tttattaata aaagaatctt taacttt 973

<210> 178
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 178
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 1 5 10 15
 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 20 25 30
 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
 85 90 95
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 100 105 110
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
 115 120 125
 Gln

<210> 179

<400> 179
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<210> 180

<400> 180
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<210> 181

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer used in the screening of cDNA encoding the protein capable of activating NF-K B

<400> 181

cttctgctct aaaagctgcg

20

<210> 182

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer used in the screening of cDNA encoding the protein capable of activating NF-K B

<400> 182

cgacctgcag ctcgagcaca

20